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(54) Title: REGULATION OF HUMAN CITRON RHO/RAC-INTERACTING KINASE

(57) Abstract: Reagents that regulate human CR1K and reagents which bind to human CR1K gene products can play a role in preventing, ameliorating, or correcting dysfunctions or diseases including, but not limited to, obesity, a CNS disorder or COPD.



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REGULATION OF HUMAN CITRON RHO/RAC-INTERACTING KINASE

This application incorporates by reference and claims the benefit of co-pending provisional applications Serial No. 60/301,841 filed July 2, 2001, Serial No.
5 60/338,651 filed December 11, 2001 and Serial No. 60/375,014 filed April 25, 2002

TECHNICAL FIELD OF THE INVENTION

The invention relates to the regulation of human citron rho/rac-interacting kinase
10 (CRIK).

BACKGROUND OF THE INVENTION

Kinases are involved in a variety of disease processes. There is a need in the art to
15 identify related enzymes, which can be regulated for therapeutic effects.

SUMMARY OF THE INVENTION

It is an object of the invention to provide reagents and methods of regulating a
20 human CRIK. This and other objects of the invention are provided by one or more of the embodiments described below.

One embodiment of the invention is a human citron rho/rac-interacting kinase polypeptide comprising an amino acid sequence selected from the group consisting
25 of:

amino acid sequences which are at least about 97% identical to the amino acid sequence shown in SEQ ID NO: 2; and

30 the amino acid sequence shown in SEQ ID NO: 2.

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Yet another embodiment of the invention is a method of screening for agents which decrease extracellular matrix degradation. A test compound is contacted with a human citron rho/rac-interacting kinase polypeptide comprising an amino acid sequence selected from the group consisting of:

5

amino acid sequences which are at least about 97% identical to the amino acid sequence shown in SEQ ID NO: 2; and

the amino acid sequence shown in SEQ ID NO: 2.

10

Binding between the test compound and the human citron rho/rac-interacting kinase polypeptide is detected. A test compound which binds to the human citron rho/rac-interacting kinase polypeptide is thereby identified as a potential agent for decreasing extracellular matrix degradation. The agent can work by decreasing the activity of the human citron rho/rac-interacting kinase.

15

Another embodiment of the invention is a method of screening for agents which decrease extracellular matrix degradation. A test compound is contacted with a polynucleotide encoding a human citron rho/rac-interacting kinase polypeptide, wherein the polynucleotide comprises a nucleotide sequence selected from the group consisting of:

20

nucleotide sequences which are at least about 50% identical to the nucleotide sequence shown in SEQ ID NO: 1;

25

the nucleotide sequence shown in SEQ ID NO: 1;

nucleotide sequences which are at least about 50% identical to the nucleotide sequence shown in SEQ ID NO: 24; and

30

the nucleotide sequence shown in SEQ ID NO: 24.

Binding of the test compound to the polynucleotide is detected. A test compound which binds to the polynucleotide is identified as a potential agent for decreasing extracellular matrix degradation. The agent can work by decreasing the amount of the human citron rho/rac-interacting kinase through interacting with the human citron rho/rac-interacting kinase mRNA.

Another embodiment of the invention is a method of screening for agents which regulate extracellular matrix degradation. A test compound is contacted with a human citron rho/rac-interacting kinase polypeptide comprising an amino acid sequence selected from the group consisting of:

amino acid sequences which are at least about 97% identical to the amino acid sequence shown in SEQ ID NO: 2; and
the amino acid sequence shown in SEQ ID NO: 2.

A human citron rho/rac-interacting kinase activity of the polypeptide is detected. A test compound which increases human citron rho/rac-interacting kinase activity of the polypeptide relative to human citron rho/rac-interacting kinase activity in the absence of the test compound is thereby identified as a potential agent for increasing extracellular matrix degradation. A test compound which decreases human citron rho/rac-interacting kinase activity of the polypeptide relative to human citron rho/rac-interacting kinase activity in the absence of the test compound is thereby identified as a potential agent for decreasing extracellular matrix degradation.

Even another embodiment of the invention is a method of screening for agents which decrease extracellular matrix degradation. A test compound is contacted with a human citron rho/rac-interacting kinase product of a polynucleotide which comprises a nucleotide sequence selected from the group consisting of:

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nucleotide sequences which are at least about 50% identical to the nucleotide sequence shown in SEQ ID NO: 1;

the nucleotide sequence shown in SEQ ID NO: 1;

5

nucleotide sequences which are at least about 50% identical to the nucleotide sequence shown in SEQ ID NO: 24; and

the nucleotide sequence shown in SEQ ID NO: 24.

10

Binding of the test compound to the human citron rho/rac-interacting kinase product is detected. A test compound which binds to the human citron rho/rac-interacting kinase product is thereby identified as a potential agent for decreasing extracellular matrix degradation.

15

Still another embodiment of the invention is a method of reducing extracellular matrix degradation. A cell is contacted with a reagent which specifically binds to a polynucleotide encoding a human citron rho/rac-interacting kinase polypeptide or the product encoded by the polynucleotide, wherein the polynucleotide comprises a nucleotide sequence selected from the group consisting of:

20

nucleotide sequences which are at least about 50% identical to the nucleotide sequence shown in SEQ ID NO: 1;

25

the nucleotide sequence shown in SEQ ID NO: 1;

nucleotide sequences which are at least about 50% identical to the nucleotide sequence shown in SEQ ID NO: 24; and

30

the nucleotide sequence shown in SEQ ID NO: 24.

Human citron rho/rac-interacting kinase activity in the cell is thereby decreased.

The invention thus provides a human CRIK that can be used to identify test compounds that may act, for example, as activators or inhibitors at the enzyme's active site. Human CRIK and fragments thereof also are useful in raising specific antibodies that can block the enzyme and effectively reduce its activity.

BRIEF DESCRIPTION OF THE DRAWINGS

- 10 Fig. 1 shows the DNA-sequence encoding a citron rho/rac-interacting kinase Polypeptide (SEQ ID NO:1).
- Fig. 2 shows the amino acid sequence deduced from the DNA-sequence of Fig.1 (SEQ ID NO:2).
- Fig. 3 shows the amino acid sequence of the protein identified
15 by trembl|AF086824|AF086824_1 (SEQ ID NO:3).
- Fig. 4 shows the DNA-sequence encoding a citron rho/rac-interacting kinase Polypeptide (SEQ ID NO:4).
- Fig. 5 shows the amino acid sequence of the protein identified by swiss|O14578|CTRO_HUMAN (SEQ ID NO:5).
- 20 Fig. 6 shows the DNA-sequence of a protein identified by trembl|AB023166|AB023166_1 (SEQ ID NO:6).
- Fig. 7 shows the amino acid sequence of the protein identified by swissnew|P54265|DMK_MOUSE (SEQ ID NO:7).
- Fig. 8 shows the BLASTP - alignment of 543_Protein (SEQ
25 ID NO:2) against trembl|AF086824|AF086824_1 (SEQ ID NO:3).
- Fig. 9 shows the BLASTP - alignment of 543_Protein (SEQ ID NO:2) against swiss|O14578|CTRO_HUMAN (SEQ ID NO:5).
- 30 Fig. 10 shows the BLASTP - alignment of 543_Protein (SEQ ID NO:2) against aageneseq|AAB43359|AAB43359.

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- Fig. 11 shows the BLASTP - alignment of 543_Protein (SEQ ID NO:2) against trembl|AB023166|AB023166_1 (SEQ ID NO:6).
- 5 Fig. 12 shows the BLASTP - alignment of 543_Protein (SEQ ID NO:2) against swissnew|P54265|DMK_MOUSE (SEQ ID NO:7).
- Fig. 13 shows the BLASTP - alignment of 543_Protein (SEQ ID NO:2) against pdb|1CDK|1CDK-A.
- 10 Fig. 14 shows the HMMPFAM - alignment of 543_Protein (SEQ ID NO:2) against pfam|hmm|pkinase.
- Fig. 15 shows the HMMPFAM - alignment of 543_Protein (SEQ ID NO:2) against pfam|hmm|PH.
- Fig. 16 shows the HMMPFAM - alignment of 543_Protein (SEQ ID NO:2) against pfam|hmm|CNH.
- 15 Fig. 17 shows the HMMPFAM - alignment of 543_Protein (SEQ ID NO:2) against pfam|hmm|DAG_PE-bind.
- Fig. 18 shows the HMMPFAM - alignment of 543_Protein (SEQ ID NO:2) against pfam|hmm|pkinase_C.
- Fig. 19 shows the Prosite search results.
- 20 Fig. 20 shows the Genewise output.
- Fig. 21 shows the Relative expression of human citron rho/rac-interacting kinase.
- Fig. 22 shows the TBLASTN - alignment of 543_Protein against emnew|AX166510|AX166510 Sequence 1 from Patent WO0138503.//:gbnew|AX166510|AX166510 Sequence Patent WO0138503.
- 25 Fig. 23 shows the TBLASTN - alignment of 543_Protein against BAYER_LIB_DNA|wu_37300600 Bayer Corp Pharma Proprietary OP Library: Fat Rat Hypothalamus
- 30 Linda Oct 15 15:45:51 EDT 1999

Fig. 24 shows the DNA-sequence encoding a citron rho/rac-interacting kinase Polypeptide.

DETAILED DESCRIPTION OF THE INVENTION

5

The invention relates to an isolated polynucleotide from the group consisting of:

- a) a polynucleotide encoding a human citron rho/rac-interacting kinase polypeptide comprising an amino acid sequence selected from the group consisting of:
10 amino acid sequences which are at least about 97% identical to the amino acid sequence shown in SEQ ID NO: 2; and the amino acid sequence shown in SEQ ID NO: 2.
- b) a polynucleotide comprising the sequence of SEQ ID NOS: 1 or 24;
- c) a polynucleotide which hybridizes under stringent conditions to a
15 polynucleotide specified in (a) and (b) and encodes a human citron rho/rac-interacting kinase polypeptide;
- d) a polynucleotide the sequence of which deviates from the polynucleotide sequences specified in (a) to (c) due to the degeneration of the genetic code and encodes a human citron rho/rac-
20 interacting kinase polypeptide; and
- e) a polynucleotide which represents a fragment, derivative or allelic variation of a polynucleotide sequence specified in (a) to (d) and encodes a human citron rho/rac-interacting kinase polypeptide.

25 Furthermore, it has been discovered by the present applicant that a novel CRIK, particularly a human CRIK, can be used in therapeutic methods to treat obesity, a CNS disorder, diabetes or COPD. Human CRIK comprises the amino acid sequence shown in SEQ ID NO:2. A coding sequence for human CRIK is shown in SEQ ID NO:1. This sequence is contained within the longer sequence shown in SEQ ID
30 NO:4, which is located on chromosome 12q24.2. Related ESTs are expressed in bone marrow, denis_drash (pediatric kidney tumors), epithelioid carcinoma

(pancreas), colon_ins (colon cancer cell line), uterus_tumor, glioblastoma with EGFR amplification, colon, nervous, nervous tumor, and bladder_tumor.

Human CRIK is 96% identical over 2056 amino acids to
 5 trembl|AF086824|AF086824_1 (SEQ ID NO:3) (FIG. 1), 100% identical over 1286
 amino acids to swiss|O14578|CTRO_HUMAN (SEQ ID NO:5) (FIG. 2), 100%
 identical over 1286 amino acids to SEQ ID NO:6246 of
 aageneseq|AAB43359|AAB43359 (FIG. 3), 100% over 940 amino acids to
 trembl|AB023166|AB023166_1 (SEQ ID NO:6) (FIG. 4), and 38% identical over
 10 522 amino acids to swissnew|P54265|DMK_MOUSE (SEQ ID NO:7) (FIG. 5).

Human CRIK of the invention is expected to be useful for the same purposes as
 previously identified CRIK enzymes. Human CRIK is believed to be useful in
 therapeutic methods to treat disorders such as CNS disorders, obesity, and COPD.
 15 Human CRIK also can be used to screen for human CRIK activators and inhibitors.

Polypeptides

Human CRIK polypeptides according to the invention comprise at least 6, 10, 15, 20,
 20 25, 50, 75, 100, 125, 150, 175, 200, 225, 250, 275, 300, 325, 350, 375, 400, 425, 450,
 475, 500, 525, 550, 575, 600, 625, 650, 675, 700, 725, 750, 775, 800, 825, 850, 875,
 900, 925, 950, 975, 1000, 1025, 1050, 1075, 1100, 1125, 1150, 1175, 1200, 1225,
 1250, 1275, 1300, 1325, 1350, 1375, 1400, 1425, 1450, 1475, 1500, 1525, 1550,
 1575, 1600, 1625, 1650, 1675, 1700, 1725, 1750, 1775, 1800, 1825, 1850, 1875,
 25 1900, 1925, 1950, 1975, 2000, 2025, 2050, or 2054 contiguous amino acids selected
 from the amino acid sequence shown in SEQ ID NO:2 or a biologically active variant
 thereof, as defined below. A CRIK polypeptide of the invention therefore can be a
 portion of a CRIK protein, a full-length CRIK protein, or a fusion protein comprising
 all or a portion of a CRIK protein.

Biologically Active Variants

Human CRIK polypeptide variants which are biologically active, *e.g.*, retain enzymatic activity, also are human CRIK polypeptides. Preferably, naturally or
5 non-naturally occurring human CRIK polypeptide variants have amino acid sequences which are at least about 97, 98, or 99% identical to the amino acid sequence shown in SEQ ID NO:2 or a fragment thereof. Percent identity between a putative human CRIK polypeptide variant and an amino acid sequence of SEQ ID NO:2 is determined by conventional methods. See, for example, Altschul *et al.*, *Bull.*
10 *Math. Bio.* 48:603 (1986), and Henikoff & Henikoff, *Proc. Natl. Acad. Sci. USA* 89:10915 (1992). Briefly, two amino acid sequences are aligned to optimize the alignment scores using a gap opening penalty of 10, a gap extension penalty of 1, and the "BLOSUM62" scoring matrix of Henikoff & Henikoff, 1992.

15 Those skilled in the art appreciate that there are many established algorithms available to align two amino acid sequences. The "FASTA" similarity search algorithm of Pearson & Lipman is a suitable protein alignment method for examining the level of identity shared by an amino acid sequence disclosed herein and the amino acid sequence of a putative variant. The FASTA algorithm is described by
20 Pearson & Lipman, *Proc. Nat'l Acad. Sci. USA* 85:2444(1988), and by Pearson, *Meth. Enzymol.* 183:63 (1990). Briefly, FASTA first characterizes sequence similarity by identifying regions shared by the query sequence (*e.g.*, SEQ ID NO: 2) and a test sequence that have either the highest density of identities (if the ktup variable is 1) or pairs of identities (if ktup=2), without considering conservative
25 amino acid substitutions, insertions, or deletions. The ten regions with the highest density of identities are then rescored by comparing the similarity of all paired amino acids using an amino acid substitution matrix, and the ends of the regions are "trimmed" to include only those residues that contribute to the highest score. If there are several regions with scores greater than the "cutoff" value (calculated by a
30 predetermined formula based upon the length of the sequence the ktup value), then the trimmed initial regions are examined to determine whether the regions can be

joined to form an approximate alignment with gaps. Finally, the highest scoring regions of the two amino acid sequences are aligned using a modification of the Needleman-Wunsch- Sellers algorithm (Needleman & Wunsch, *J. Mol. Biol.*48:444 (1970); Sellers, *SIAM J. Appl. Math.*26:787 (1974)), which allows for amino acid
5 insertions and deletions. Preferred parameters for FASTA analysis are: ktup=1, gap opening penalty=10, gap extension penalty=1, and substitution matrix=BLOSUM62. These parameters can be introduced into a FASTA program by modifying the scoring matrix file ("SMATRIX"), as explained in Appendix 2 of Pearson, *Meth. Enzymol.* 183:63 (1990).

10 FASTA can also be used to determine the sequence identity of nucleic acid molecules using a ratio as disclosed above. For nucleotide sequence comparisons, the ktup value can range between one to six, preferably from three to six, most preferably three, with other parameters set as default.

15 Variations in percent identity can be due, for example, to amino acid substitutions, insertions, or deletions. Amino acid substitutions are defined as one for one amino acid replacements. They are conservative in nature when the substituted amino acid has similar structural and/or chemical properties. Examples of conservative
20 replacements are substitution of a leucine with an isoleucine or valine, an aspartate with a glutamate, or a threonine with a serine.

Amino acid insertions or deletions are changes to or within an amino acid sequence. They typically fall in the range of about 1 to 5 amino acids. Guidance in determining
25 which amino acid residues can be substituted, inserted, or deleted without abolishing biological or immunological activity of a human CRIK polypeptide can be found using computer programs well known in the art, such as DNASTAR software.

30 The invention additionally, encompasses CRIK polypeptides that are differentially modified during or after translation, *e.g.*, by glycosylation, acetylation, phosphorylation, amidation, derivatization by known protecting/blocking groups,

proteolytic cleavage, linkage to an antibody molecule or other cellular ligand, etc. Any of numerous chemical modifications can be carried out by known techniques including, but not limited, to specific chemical cleavage by cyanogen bromide, trypsin, chymotrypsin, papain, V8 protease, NaBH₄, acetylation, formylation, oxidation, reduction, metabolic synthesis in the presence of tunicamycin, etc.

Additional post-translational modifications encompassed by the invention include, for example, *e.g.*, N-linked or O-linked carbohydrate chains, processing of N-terminal or C-terminal ends), attachment of chemical moieties to the amino acid backbone, chemical modifications of N-linked or O-linked carbohydrate chains, and addition or deletion of an N-terminal methionine residue as a result of prokaryotic host cell expression. The CRIK polypeptides may also be modified with a detectable label, such as an enzymatic, fluorescent, isotopic or affinity label to allow for detection and isolation of the protein.

The invention also provides chemically modified derivatives of CRIK polypeptides that may provide additional advantages such as increased solubility, stability and circulating time of the polypeptide, or decreased immunogenicity (see U.S. Patent No. 4,179,337). The chemical moieties for derivitization can be selected from water soluble polymers such as polyethylene glycol, ethylene glycol/propylene glycol copolymers, carboxymethylcellulose, dextran, polyvinyl alcohol, and the like. The polypeptides can be modified at random or predetermined positions within the molecule and can include one, two, three, or more attached chemical moieties.

Whether an amino acid change or a polypeptide modification results in a biologically active CRIK polypeptide can readily be determined by assaying for enzymatic activity, as described for example, in Di Cunto F. *et al.*, J Biol Chem. 1998 Nov 6;273(45):29706-11.

Fusion Proteins

Fusion proteins are useful for generating antibodies against CRIK polypeptide amino acid sequences and for use in various assay systems. For example, fusion proteins can be used to identify proteins that interact with portions of a CRIK polypeptide. Protein affinity chromatography or library-based assays for protein-protein interactions, such as the yeast two-hybrid or phage display systems, can be used for this purpose. Such methods are well known in the art and also can be used as drug screens.

A CRIK polypeptide fusion protein comprises two polypeptide segments fused together by means of a peptide bond. The first polypeptide segment comprises at least 6, 10, 15, 20, 25, 50, 75, 100, 125, 150, 175, 200, 225, 250, 275, 300, 325, 350, 375, 400, 425, 450, 475, 500, 525, 550, 575, 600, 625, 650, 675, 700, 725, 750, 775, 800, 825, 850, 875, 900, 925, 950, 975, 1000, 1025, 1050, 1075, 1100, 1125, 1150, 1175, 1200, 1225, 1250, 1275, 1300, 1325, 1350, 1375, 1400, 1425, 1450, 1475, 1500, 1525, 1550, 1575, 1600, 1625, 1650, 1675, 1700, 1725, 1750, 1775, 1800, 1825, 1850, 1875, 1900, 1925, 1950, 1975, 2000, 2025, 2050, or 2054 contiguous amino acids of SEQ ID NO:2 or of a biologically active variant, such as those described above. The first polypeptide segment also can comprise full-length CRIK protein.

The second polypeptide segment can be a full-length protein or a protein fragment. Proteins commonly used in fusion protein construction include β -galactosidase, β -glucuronidase, green fluorescent protein (GFP), autofluorescent proteins, including blue fluorescent protein (BFP), glutathione-S-transferase (GST), luciferase, horseradish peroxidase (HRP), and chloramphenicol acetyltransferase (CAT). Additionally, epitope tags are used in fusion protein constructions, including histidine (His) tags, FLAG tags, influenza hemagglutinin (HA) tags, Myc tags, VSV-G tags, and thioredoxin (Trx) tags. Other fusion constructions can include maltose binding protein (MBP), S-tag, Lex a DNA binding domain (DBD) fusions, GAL4

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DNA binding domain fusions, and herpes simplex virus (HSV) BP16 protein fusions. A fusion protein also can be engineered to contain a cleavage site located between the CRIK polypeptide-encoding sequence and the heterologous protein sequence, so that the CRIK polypeptide can be cleaved and purified away from the heterologous moiety.

A fusion protein can be synthesized chemically, as is known in the art. Preferably, a fusion protein is produced by covalently linking two polypeptide segments or by standard procedures in the art of molecular biology. Recombinant DNA methods can be used to prepare fusion proteins, for example, by making a DNA construct which comprises coding sequences selected from SEQ ID NO:1 in proper reading frame with nucleotides encoding the second polypeptide segment and expressing the DNA construct in a host cell, as is known in the art. Many kits for constructing fusion proteins are available from companies such as Promega Corporation (Madison, WI), Stratagene (La Jolla, CA), CLONTECH (Mountain View, CA), Santa Cruz Biotechnology (Santa Cruz, CA), MBL International Corporation (MIC; Watertown, MA), and Quantum Biotechnologies (Montreal, Canada; 1-888-DNA-KITS).

Identification of Species Homologs

Species homologs of human CRIK polypeptide can be obtained using CRIK polypeptide polynucleotides (described below) to make suitable probes or primers for screening cDNA expression libraries from other species, such as mice, monkeys, or yeast, identifying cDNAs which encode homologs of CRIK polypeptide, and expressing the cDNAs as is known in the art.

Polynucleotides

A CRIK polynucleotide can be single- or double-stranded and comprises a coding sequence or the complement of a coding sequence for a CRIK polypeptide. A coding sequence for human CRIK is shown in SEQ ID NO:1.

Degenerate nucleotide sequences encoding human CRIK polypeptides, as well as homologous nucleotide sequences which are at least about 50, 55, 60, 65, 70, preferably about 75, 90, 96, 98, or 99% identical to the nucleotide sequence shown in SEQ ID NO:1 or its complement also are CRIK polynucleotides. Percent sequence identity between the sequences of two polynucleotides is determined using computer programs such as ALIGN which employ the FASTA algorithm, using an affine gap search with a gap open penalty of -12 and a gap extension penalty of -2. Complementary DNA (cDNA) molecules, species homologs, and variants of CRIK polynucleotides that encode biologically active CRIK polypeptides also are CRIK polynucleotides. Polynucleotide fragments comprising at least 8, 9, 10, 11, 12, 15, 20, or 25 contiguous nucleotides of SEQ ID NO:1 or its complement also are CRIK polynucleotides. These fragments can be used, for example, as hybridization probes or as antisense oligonucleotides.

Identification of Polynucleotide Variants and Homologs

Variants and homologs of the CRIK polynucleotides described above also are CRIK polynucleotides. Typically, homologous CRIK polynucleotide sequences can be identified by hybridization of candidate polynucleotides to known CRIK polynucleotides under stringent conditions, as is known in the art. For example, using the following wash conditions--2X SSC (0.3 M NaCl, 0.03 M sodium citrate, pH 7.0), 0.1% SDS, room temperature twice, 30 minutes each; then 2X SSC, 0.1% SDS, 50 °C once, 30 minutes; then 2X SSC, room temperature twice, 10 minutes each--homologous sequences can be identified which contain at most about 25-30%

basepair mismatches. More preferably, homologous nucleic acid strands contain 15-25% basepair mismatches, even more preferably 5-15% basepair mismatches.

Species homologs of the CRIK polynucleotides disclosed herein also can be identified by making suitable probes or primers and screening cDNA expression libraries from other species, such as mice, monkeys, or yeast. Human variants of CRIK polynucleotides can be identified, for example, by screening human cDNA expression libraries. It is well known that the T_m of a double-stranded DNA decreases by 1-1.5 °C with every 1% decrease in homology (Bonner *et al.*, *J. Mol. Biol.* 81, 123 (1973). Variants of human CRIK polynucleotides or CRIK polynucleotides of other species can therefore be identified by hybridizing a putative homologous CRIK polynucleotide with a polynucleotide having a nucleotide sequence of SEQ ID NO:1 or the complement thereof to form a test hybrid. The melting temperature of the test hybrid is compared with the melting temperature of a hybrid comprising polynucleotides having perfectly complementary nucleotide sequences, and the number or percent of basepair mismatches within the test hybrid is calculated.

Nucleotide sequences which hybridize to CRIK polynucleotides or their complements following stringent hybridization and/or wash conditions also are CRIK polynucleotides. Stringent wash conditions are well known and understood in the art and are disclosed, for example, in Sambrook *et al.*, MOLECULAR CLONING: A LABORATORY MANUAL, 2d ed., 1989, at pages 9.50-9.51.

Typically, for stringent hybridization conditions a combination of temperature and salt concentration should be chosen that is approximately 12-20 °C below the calculated T_m of the hybrid under study. The T_m of a hybrid between a CRIK polynucleotide having a nucleotide sequence shown in SEQ ID NO:1 or the complement thereof and a polynucleotide sequence which is at least about 50, preferably about 75, 90, 96, or 98% identical to one of those nucleotide sequences

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can be calculated, for example, using the equation of Bolton and McCarthy, *Proc. Natl. Acad. Sci. U.S.A.* 48, 1390 (1962):

$$T_m = 81.5\text{ }^{\circ}\text{C} - 16.6(\log_{10}[\text{Na}^+]) + 0.41(\%G + C) - 0.63(\%\text{formamide}) - 600/l,$$

5 where l = the length of the hybrid in basepairs.

Stringent wash conditions include, for example, 4X SSC at 65 °C, or 50% formamide, 4X SSC at 42 °C, or 0.5X SSC, 0.1% SDS at 65 °C. Highly stringent wash conditions include, for example, 0.2X SSC at 65 °C.

10

Preparation of Polynucleotides

A CRIK polynucleotide can be isolated free of other cellular components such as membrane components, proteins, and lipids. Polynucleotides can be made by a cell and isolated using standard nucleic acid purification techniques, or synthesized using an amplification technique, such as the polymerase chain reaction (PCR), or by using an automatic synthesizer. Methods for isolating polynucleotides are routine and are known in the art. Any such technique for obtaining a polynucleotide can be used to obtain isolated CRIK polynucleotides. For example, restriction enzymes and probes can be used to isolate polynucleotide fragments, which comprise CRIK nucleotide sequences. Isolated polynucleotides are in preparations that are free or at least 70, 80, or 90% free of other molecules.

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Human CRIK cDNA molecules can be made with standard molecular biology techniques, using CRIK mRNA as a template. Human CRIK cDNA molecules can thereafter be replicated using molecular biology techniques known in the art and disclosed in manuals such as Sambrook *et al.* (1989). An amplification technique, such as PCR, can be used to obtain additional copies of polynucleotides of the invention, using either human genomic DNA or cDNA as a template.

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Alternatively, synthetic chemistry techniques can be used to synthesize CRIK polynucleotides. The degeneracy of the genetic code allows alternate nucleotide sequences to be synthesized which will encode a CRIK polypeptide having, for example, an amino acid sequence shown in SEQ ID NO:2 or a biologically active variant thereof.

Extending Polynucleotides

Various PCR-based methods can be used to extend the nucleic acid sequences disclosed herein to detect upstream sequences such as promoters and regulatory elements. For example, restriction-site PCR uses universal primers to retrieve unknown sequence adjacent to a known locus (Sarkar, *PCR Methods Applic.* 2, 318-322, 1993). Genomic DNA is first amplified in the presence of a primer to a linker sequence and a primer specific to the known region. The amplified sequences are then subjected to a second round of PCR with the same linker primer and another specific primer internal to the first one. Products of each round of PCR are transcribed with an appropriate RNA polymerase and sequenced using reverse transcriptase.

Inverse PCR also can be used to amplify or extend sequences using divergent primers based on a known region (Triglia *et al.*, *Nucleic Acids Res.* 16, 8186, 1988). Primers can be designed using commercially available software, such as OLIGO 4.06 Primer Analysis software (National Biosciences Inc., Plymouth, Minn.), to be 22-30 nucleotides in length, to have a GC content of 50% or more, and to anneal to the target sequence at temperatures about 68-72 °C. The method uses several restriction enzymes to generate a suitable fragment in the known region of a gene. The fragment is then circularized by intramolecular ligation and used as a PCR template.

Another method which can be used is capture PCR, which involves PCR amplification of DNA fragments adjacent to a known sequence in human and yeast artificial chromosome DNA (Lagerstrom *et al.*, *PCR Methods Applic.* 1, 111-119,

1991). In this method, multiple restriction enzyme digestions and ligations also can be used to place an engineered double-stranded sequence into an unknown fragment of the DNA molecule before performing PCR.

5 Another method which can be used to retrieve unknown sequences is that of Parker *et al.*, *Nucleic Acids Res.* 19, 3055-3060, 1991). Additionally, PCR, nested primers, and PROMOTERFINDER libraries (CLONTECH, Palo Alto, Calif.) can be used to walk genomic DNA (CLONTECH, Palo Alto, Calif.). This process avoids the need to screen libraries and is useful in finding intron/exon junctions.

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When screening for full-length cDNAs, it is preferable to use libraries that have been size-selected to include larger cDNAs. Randomly-primed libraries are preferable, in that they will contain more sequences which contain the 5' regions of genes. Use of a randomly primed library may be especially preferable for situations in which an
15 oligo d(T) library does not yield a full-length cDNA. Genomic libraries can be useful for extension of sequence into 5' non-transcribed regulatory regions.

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Commercially available capillary electrophoresis systems can be used to analyze the size or confirm the nucleotide sequence of PCR or sequencing products. For
example, capillary sequencing can employ flowable polymers for electrophoretic separation, four different fluorescent dyes (one for each nucleotide) that are laser activated, and detection of the emitted wavelengths by a charge coupled device camera. Output/light intensity can be converted to electrical signal using appropriate software (*e.g.* GENOTYPER and Sequence NAVIGATOR, Perkin Elmer), and the
25 entire process from loading of samples to computer analysis and electronic data display can be computer controlled. Capillary electrophoresis is especially preferable for the sequencing of small pieces of DNA that might be present in limited amounts in a particular sample.

Obtaining Polypeptides

Human CRIK polypeptides can be obtained, for example, by purification from human cells, by expression of CRIK polynucleotides, or by direct chemical synthesis.

5

Protein Purification

Human CRIK polypeptides can be purified from any cell that expresses the polypeptide, including host cells that have been transfected with CRIK expression constructs. A purified CRIK polypeptide is separated from other compounds that normally associate with the CRIK polypeptide in the cell, such as certain proteins, carbohydrates, or lipids, using methods well-known in the art. Such methods include, but are not limited to, size exclusion chromatography, ammonium sulfate fractionation, ion exchange chromatography, affinity chromatography, and preparative gel electrophoresis. A preparation of purified CRIK polypeptides is at least 80% pure; preferably, the preparations are 90%, 95%, or 99% pure. Purity of the preparations can be assessed by any means known in the art, such as SDS-polyacrylamide gel electrophoresis.

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Expression of Polynucleotides

To express a CRIK polynucleotide, the polynucleotide can be inserted into an expression vector that contains the necessary elements for the transcription and translation of the inserted coding sequence. Methods that are well known to those skilled in the art can be used to construct expression vectors containing sequences encoding CRIK polypeptides and appropriate transcriptional and translational control elements. These methods include *in vitro* recombinant DNA techniques, synthetic techniques, and *in vivo* genetic recombination. Such techniques are described, for example, in Sambrook *et al.* (1989) and in Ausubel *et al.*, CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, New York, N.Y., 1989.

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A variety of expression vector/host systems can be utilized to contain and express sequences encoding a CRIK polypeptide. These include, but are not limited to, microorganisms, such as bacteria transformed with recombinant bacteriophage, plasmid, or cosmid DNA expression vectors; yeast transformed with yeast expression
5 vectors, insect cell systems infected with virus expression vectors (*e.g.*, baculovirus), plant cell systems transformed with virus expression vectors (*e.g.*, cauliflower mosaic virus, CaMV; tobacco mosaic virus, TMV) or with bacterial expression vectors (*e.g.*, Ti or pBR322 plasmids), or animal cell systems.

10 The control elements or regulatory sequences are those non-translated regions of the vector -- enhancers, promoters, 5' and 3' untranslated regions -- which interact with host cellular proteins to carry out transcription and translation. Such elements can vary in their strength and specificity. Depending on the vector system and host
15 utilized, any number of suitable transcription and translation elements, including constitutive and inducible promoters, can be used. For example, when cloning in bacterial systems, inducible promoters such as the hybrid *lacZ* promoter of the BLUESCRIPT phagemid (Stratagene, LaJolla, Calif.) or pSPORT1 plasmid (Life Technologies) and the like can be used. The baculovirus polyhedrin promoter can be used in insect cells. Promoters or enhancers derived from the genomes of plant
20 cells (*e.g.*, heat shock, RUBISCO, and storage protein genes) or from plant viruses (*e.g.*, viral promoters or leader sequences) can be cloned into the vector. In mammalian cell systems, promoters from mammalian genes or from mammalian viruses are preferable. If it is necessary to generate a cell line that contains multiple copies of a nucleotide sequence encoding a CRIK polypeptide, vectors based on
25 SV40 or EBV can be used with an appropriate selectable marker.

Bacterial and Yeast Expression Systems

30 In bacterial systems, a number of expression vectors can be selected depending upon the use intended for the CRIK polypeptide. For example, when a large quantity of a CRIK polypeptide is needed for the induction of antibodies, vectors which direct

high level expression of fusion proteins that are readily purified can be used. Such vectors include, but are not limited to, multifunctional *E. coli* cloning and expression vectors such as BLUESCRIPT (Stratagene). In a BLUESCRIPT vector, a sequence encoding the CRIK polypeptide can be ligated into the vector in frame with sequences for the amino-terminal Met and the subsequent 7 residues of β -galactosidase so that a hybrid protein is produced. pIN vectors (Van Heeke & Schuster, *J. Biol. Chem.* 264, 5503-5509, 1989) or pGEX vectors (Promega, Madison, Wis.) also can be used to express foreign polypeptides as fusion proteins with glutathione S-transferase (GST). In general, such fusion proteins are soluble and can easily be purified from lysed cells by adsorption to glutathione-agarose beads followed by elution in the presence of free glutathione. Proteins made in such systems can be designed to include heparin, thrombin, or factor Xa protease cleavage sites so that the cloned polypeptide of interest can be released from the GST moiety at will.

In the yeast *Saccharomyces cerevisiae*, a number of vectors containing constitutive or inducible promoters such as alpha factor, alcohol oxidase, and PGH can be used. For reviews, see Ausubel *et al.* (1989) and Grant *et al.*, *Methods Enzymol.* 153, 516-544, 1987.

Plant and Insect Expression Systems

If plant expression vectors are used, the expression of sequences encoding CRIK polypeptides can be driven by any of a number of promoters. For example, viral promoters such as the 35S and 19S promoters of CaMV can be used alone or in combination with the omega leader sequence from TMV (Takamatsu, *EMBO J.* 6, 307-311, 1987). Alternatively, plant promoters such as the small subunit of RUBISCO or heat shock promoters can be used (Coruzzi *et al.*, *EMBO J.* 3, 1671-1680, 1984; Broglie *et al.*, *Science* 224, 838-843, 1984; Winter *et al.*, *Results Probl. Cell Differ.* 17, 85-105, 1991). These constructs can be introduced into plant cells by direct DNA transformation or by pathogen-mediated transfection. Such

techniques are described in a number of generally available reviews (*e.g.*, Hobbs or Murray, in MCGRAW HILL YEARBOOK OF SCIENCE AND TECHNOLOGY, McGraw Hill, New York, N.Y., pp. 191-196, 1992).

5 An insect system also can be used to express a CRIK polypeptide. For example, in one such system *Autographa californica* nuclear polyhedrosis virus (AcNPV) is used as a vector to express foreign genes in *Spodoptera frugiperda* cells or in *Trichoplusia* larvae. Sequences encoding CRIK polypeptides can be cloned into a non-essential region of the virus, such as the polyhedrin gene, and placed under control of the
10 polyhedrin promoter. Successful insertion of CRIK polypeptides will render the polyhedrin gene inactive and produce recombinant virus lacking coat protein. The recombinant viruses can then be used to infect *S. frugiperda* cells or *Trichoplusia* larvae in which CRIK polypeptides can be expressed (Engelhard *et al.*, *Proc. Nat. Acad. Sci.* 91, 3224-3227, 1994).

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Mammalian Expression Systems

A number of viral-based expression systems can be used to express CRIK polypeptides in mammalian host cells. For example, if an adenovirus is used as an
20 expression vector, sequences encoding CRIK polypeptides can be ligated into an adenovirus transcription/translation complex comprising the late promoter and tripartite leader sequence. Insertion in a non-essential E1 or E3 region of the viral genome can be used to obtain a viable virus that is capable of expressing a CRIK polypeptide in infected host cells (Logan & Shenk, *Proc. Natl. Acad. Sci.* 81, 3655-3659, 1984). If desired, transcription enhancers, such as the Rous sarcoma
25 virus (RSV) enhancer, can be used to increase expression in mammalian host cells.

Human artificial chromosomes (HACs) also can be used to deliver larger fragments of DNA than can be contained and expressed in a plasmid. HACs of 6M to 10M are
30 constructed and delivered to cells via conventional delivery methods (*e.g.*, liposomes, polycationic amino polymers, or vesicles).

Specific initiation signals also can be used to achieve more efficient translation of sequences encoding CRIK polypeptides. Such signals include the ATG initiation codon and adjacent sequences. In cases where sequences encoding a CRIK polypeptide, its initiation codon, and upstream sequences are inserted into the appropriate expression vector, no additional transcriptional or translational control signals may be needed. However, in cases where only coding sequence, or a fragment thereof, is inserted, exogenous translational control signals (including the ATG initiation codon) should be provided. The initiation codon should be in the correct reading frame to ensure translation of the entire insert. Exogenous translational elements and initiation codons can be of various origins, both natural and synthetic. The efficiency of expression can be enhanced by the inclusion of enhancers which are appropriate for the particular cell system which is used (see Scharf *et al.*, *Results Probl. Cell Differ.* 20, 125-162, 1994).

Host Cells

A host cell strain can be chosen for its ability to modulate the expression of the inserted sequences or to process the expressed CRIK polypeptide in the desired fashion. Such modifications of the polypeptide include, but are not limited to, acetylation, carboxylation, glycosylation, phosphorylation, lipidation, and acylation. Post-translational processing which cleaves a "prepro" form of the polypeptide also can be used to facilitate correct insertion, folding and/or function. Different host cells that have specific cellular machinery and characteristic mechanisms for post-translational activities (*e.g.*, CHO, HeLa, MDCK, HEK293, and WI38), are available from the American Type Culture Collection (ATCC; 10801 University Boulevard, Manassas, VA 20110-2209) and can be chosen to ensure the correct modification and processing of the foreign protein.

Stable expression is preferred for long-term, high-yield production of recombinant proteins. For example, cell lines which stably express CRIK polypeptides can be

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transformed using expression vectors which can contain viral origins of replication and/or endogenous expression elements and a selectable marker gene on the same or on a separate vector. Following the introduction of the vector, cells can be allowed to grow for 1-2 days in an enriched medium before they are switched to a selective medium. The purpose of the selectable marker is to confer resistance to selection, and its presence allows growth and recovery of cells which successfully express the introduced CRIK sequences. Resistant clones of stably transformed cells can be proliferated using tissue culture techniques appropriate to the cell type. See, for example, ANIMAL CELL CULTURE, R.I. Freshney, ed., 1986.

Any number of selection systems can be used to recover transformed cell lines.

These include, but are not limited to, the herpes simplex virus thymidine kinase (Wigler *et al.*, *Cell* 11, 223-32, 1977) and adenine phosphoribosyltransferase (Lowy *et al.*, *Cell* 22, 817-23, 1980) genes which can be employed in *tk⁻* or *aprt⁻* cells, respectively. Also, antimetabolite, antibiotic, or herbicide resistance can be used as the basis for selection. For example, *dhfr* confers resistance to methotrexate (Wigler *et al.*, *Proc. Natl. Acad. Sci.* 77, 3567-70, 1980), *npt* confers resistance to the aminoglycosides, neomycin and G-418 (Colbere-Garapin *et al.*, *J. Mol. Biol.* 150, 1-14, 1981), and *als* and *pat* confer resistance to chlorsulfuron and phosphinotricin acetyltransferase, respectively (Murray, 1992, *supra*). Additional selectable genes have been described. For example, *trpB* allows cells to utilize indole in place of tryptophan, or *hisD*, which allows cells to utilize histinol in place of histidine (Hartman & Mulligan, *Proc. Natl. Acad. Sci.* 85, 8047-51, 1988). Visible markers such as anthocyanins, β -glucuronidase and its substrate GUS, and luciferase and its substrate luciferin, can be used to identify transformants and to quantify the amount of transient or stable protein expression attributable to a specific vector system (Rhodes *et al.*, *Methods Mol. Biol.* 55, 121-131, 1995).

Detecting Expression

Although the presence of marker gene expression suggests that the CRIK polynucleotide is also present, its presence and expression may need to be confirmed. For example, if a sequence encoding a CRIK polypeptide is inserted within a marker gene sequence, transformed cells containing sequences that encode a CRIK polypeptide can be identified by the absence of marker gene function. Alternatively, a marker gene can be placed in tandem with a sequence encoding a CRIK polypeptide under the control of a single promoter. Expression of the marker gene in response to induction or selection usually indicates expression of the CRIK polynucleotide.

Alternatively, host cells which contain a CRIK polynucleotide and which express a CRIK polypeptide can be identified by a variety of procedures known to those of skill in the art. These procedures include, but are not limited to, DNA-DNA or DNA-RNA hybridizations and protein bioassay or immunoassay techniques that include membrane, solution, or chip-based technologies for the detection and/or quantification of nucleic acid or protein. For example, the presence of a polynucleotide sequence encoding a CRIK polypeptide can be detected by DNA-DNA or DNA-RNA hybridization or amplification using probes or fragments or fragments of polynucleotides encoding a CRIK polypeptide. Nucleic acid amplification-based assays involve the use of oligonucleotides selected from sequences encoding a CRIK polypeptide to detect transformants that contain a CRIK polynucleotide.

A variety of protocols for detecting and measuring the expression of a CRIK polypeptide, using either polyclonal or monoclonal antibodies specific for the polypeptide, are known in the art. Examples include enzyme-linked immunosorbent assay (ELISA), radioimmunoassay (RIA), and fluorescence activated cell sorting (FACS). A two-site, monoclonal-based immunoassay using monoclonal antibodies reactive to two non-interfering epitopes on a CRIK polypeptide can be used, or a competitive binding assay can be employed. These and other assays are described in Hampton *et*

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al., SEROLOGICAL METHODS: A LABORATORY MANUAL, APS Press, St. Paul, Minn., 1990) and Maddox *et al.*, *J. Exp. Med.* 158, 1211-1216, 1983).

5 A wide variety of labels and conjugation techniques are known by those skilled in the art and can be used in various nucleic acid and amino acid assays. Means for producing labeled hybridization or PCR probes for detecting sequences related to polynucleotides encoding CRIK polypeptides include oligolabeling, nick translation, end-labeling, or PCR amplification using a labeled nucleotide. Alternatively, sequences encoding a CRIK polypeptide can be cloned into a vector for the production
10 of an mRNA probe. Such vectors are known in the art, are commercially available, and can be used to synthesize RNA probes *in vitro* by addition of labeled nucleotides and an appropriate RNA polymerase such as T7, T3, or SP6. These procedures can be conducted using a variety of commercially available kits (Amersham Pharmacia Biotech, Promega, and US Biochemical). Suitable reporter molecules or labels
15 which can be used for ease of detection include radionuclides, enzymes, and fluorescent, chemiluminescent, or chromogenic agents, as well as substrates, co-factors, inhibitors, magnetic particles, and the like.

Expression and Purification of Polypeptides

20 Host cells transformed with nucleotide sequences encoding a CRIK polypeptide can be cultured under conditions suitable for the expression and recovery of the protein from cell culture. The polypeptide produced by a transformed cell can be secreted or contained intracellularly depending on the sequence and/or the vector used. As will
25 be understood by those of skill in the art, expression vectors containing polynucleotides which encode CRIK polypeptides can be designed to contain signal sequences which direct secretion of soluble CRIK polypeptides through a prokaryotic or eukaryotic cell membrane or which direct the membrane insertion of membrane-bound CRIK polypeptide.

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As discussed above, other constructions can be used to join a sequence encoding a CRIK polypeptide to a nucleotide sequence encoding a polypeptide domain which will facilitate purification of soluble proteins. Such purification facilitating domains include, but are not limited to, metal chelating peptides such as histidine-tryptophan modules that allow purification on immobilized metals, protein A domains that allow purification on immobilized immunoglobulin, and the domain utilized in the FLAGS extension/affinity purification system (Immunex Corp., Seattle, Wash.). Inclusion of cleavable linker sequences such as those specific for Factor Xa or enterokinase (Invitrogen, San Diego, CA) between the purification domain and the CRIK polypeptide also can be used to facilitate purification. One such expression vector provides for expression of a fusion protein containing a CRIK polypeptide and 6 histidine residues preceding a thioredoxin or an enterokinase cleavage site. The histidine residues facilitate purification by IMAC (immobilized metal ion affinity chromatography, as described in Porath *et al.*, *Prot. Exp. Purif.* 3, 263-281, 1992), while the enterokinase cleavage site provides a means for purifying the CRIK polypeptide from the fusion protein. Vectors that contain fusion proteins are disclosed in Kroll *et al.*, *DNA Cell Biol.* 12, 441-453, 1993.

Chemical Synthesis

Sequences encoding a CRIK polypeptide can be synthesized, in whole or in part, using chemical methods well known in the art (see Caruthers *et al.*, *Nucl. Acids Res. Symp. Ser.* 215-223, 1980; Horn *et al.* *Nucl. Acids Res. Symp. Ser.* 225-232, 1980). Alternatively, a CRIK polypeptide itself can be produced using chemical methods to synthesize its amino acid sequence, such as by direct peptide synthesis using solid-phase techniques (Merrifield, *J. Am. Chem. Soc.* 85, 2149-2154, 1963; Roberge *et al.*, *Science* 269, 202-204, 1995). Protein synthesis can be performed using manual techniques or by automation. Automated synthesis can be achieved, for example, using Applied Biosystems 431A Peptide Synthesizer (Perkin Elmer). Optionally, fragments of CRIK polypeptides can be separately synthesized and combined using chemical methods to produce a full-length molecule.

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The newly synthesized peptide can be substantially purified by preparative high performance liquid chromatography (*e.g.*, Creighton, PROTEINS: STRUCTURES AND MOLECULAR PRINCIPLES, WH Freeman and Co., New York, N.Y., 1983). The composition of a synthetic CRIK polypeptide can be confirmed by amino acid analysis or sequencing (*e.g.*, the Edman degradation procedure; *see* Creighton, *supra*). Additionally, any portion of the amino acid sequence of the CRIK polypeptide can be altered during direct synthesis and/or combined using chemical methods with sequences from other proteins to produce a variant polypeptide or a fusion protein.

Production of Altered Polypeptides

As will be understood by those of skill in the art, it may be advantageous to produce CRIK polypeptide-encoding nucleotide sequences possessing non-naturally occurring codons. For example, codons preferred by a particular prokaryotic or eukaryotic host can be selected to increase the rate of protein expression or to produce an RNA transcript having desirable properties, such as a half-life that is longer than that of a transcript generated from the naturally occurring sequence.

The nucleotide sequences disclosed herein can be engineered using methods generally known in the art to alter CRIK polypeptide-encoding sequences for a variety of reasons, including but not limited to, alterations which modify the cloning, processing, and/or expression of the polypeptide or mRNA product. DNA shuffling by random fragmentation and PCR reassembly of gene fragments and synthetic oligonucleotides can be used to engineer the nucleotide sequences. For example, site-directed mutagenesis can be used to insert new restriction sites, alter glycosylation patterns, change codon preference, produce splice variants, introduce mutations, and so forth.

30

Antibodies

Any type of antibody known in the art can be generated to bind specifically to an epitope of a CRIK polypeptide. "Antibody" as used herein includes intact immunoglobulin molecules, as well as fragments thereof, such as Fab, F(ab')₂, and Fv, which are capable of binding an epitope of a CRIK polypeptide. Typically, at least 6, 8, 10, or 12 contiguous amino acids are required to form an epitope. However, epitopes which involve non-contiguous amino acids may require more, *e.g.*, at least 15, 25, or 50 amino acids.

An antibody which specifically binds to an epitope of a CRIK polypeptide can be used therapeutically, as well as in immunochemical assays, such as Western blots, ELISAs, radioimmunoassays, immunohistochemical assays, immunoprecipitations, or other immunochemical assays known in the art. Various immunoassays can be used to identify antibodies having the desired specificity. Numerous protocols for competitive binding or immunoradiometric assays are well known in the art. Such immunoassays typically involve the measurement of complex formation between an immunogen and an antibody that specifically binds to the immunogen.

Typically, an antibody which specifically binds to a CRIK polypeptide provides a detection signal at least 5-, 10-, or 20-fold higher than a detection signal provided with other proteins when used in an immunochemical assay. Preferably, antibodies which specifically bind to CRIK polypeptides do not detect other proteins in immunochemical assays and can immunoprecipitate a CRIK polypeptide from solution.

Human CRIK polypeptides can be used to immunize a mammal, such as a mouse, rat, rabbit, guinea pig, monkey, or human, to produce polyclonal antibodies. If desired, a CRIK polypeptide can be conjugated to a carrier protein, such as bovine serum albumin, thyroglobulin, and keyhole limpet hemocyanin. Depending on the host species, various adjuvants can be used to increase the immunological response.

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Such adjuvants include, but are not limited to, Freund's adjuvant, mineral gels (e.g., aluminum hydroxide), and surface active substances (e.g. lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, keyhole limpet hemocyanin, and dinitrophenol). Among adjuvants used in humans, BCG (*bacilli Calmette-Guerin*) and *Corynebacterium parvum* are especially useful.

Monoclonal antibodies that specifically bind to a CRIK polypeptide can be prepared using any technique which provides for the production of antibody molecules by continuous cell lines in culture. These techniques include, but are not limited to, the hybridoma technique, the human B-cell hybridoma technique, and the EBV-hybridoma technique (Kohler *et al.*, *Nature* 256, 495-497, 1985; Kozbor *et al.*, *J. Immunol. Methods* 81, 31-42, 1985; Cote *et al.*, *Proc. Natl. Acad. Sci.* 80, 2026-2030, 1983; Cole *et al.*, *Mol. Cell Biol.* 62, 109-120, 1984).

In addition, techniques developed for the production of "chimeric antibodies," the splicing of mouse antibody genes to human antibody genes to obtain a molecule with appropriate antigen specificity and biological activity, can be used (Morrison *et al.*, *Proc. Natl. Acad. Sci.* 81, 6851-6855, 1984; Neuberger *et al.*, *Nature* 312, 604-608, 1984; Takeda *et al.*, *Nature* 314, 452-454, 1985). Monoclonal and other antibodies also can be "humanized" to prevent a patient from mounting an immune response against the antibody when it is used therapeutically. Such antibodies may be sufficiently similar in sequence to human antibodies to be used directly in therapy or may require alteration of a few key residues. Sequence differences between rodent antibodies and human sequences can be minimized by replacing residues which differ from those in the human sequences by site directed mutagenesis of individual residues or by grating of entire complementarity determining regions. Alternatively, humanized antibodies can be produced using recombinant methods, as described in GB2188638B. Antibodies that specifically bind to a CRIK polypeptide can contain antigen binding sites which are either partially or fully humanized, as disclosed in U.S. 5,565,332.

Alternatively, techniques described for the production of single chain antibodies can be adapted using methods known in the art to produce single chain antibodies that specifically bind to CRIK polypeptides. Antibodies with related specificity, but of distinct idiotypic composition, can be generated by chain shuffling from random combinatorial immunoglobulin libraries (Burton, *Proc. Natl. Acad. Sci.* 88, 11120-23, 1991).

Single-chain antibodies also can be constructed using a DNA amplification method, such as PCR, using hybridoma cDNA as a template (Thirion *et al.*, 1996, *Eur. J. Cancer Prev.* 5, 507-11). Single-chain antibodies can be mono- or bispecific, and can be bivalent or tetravalent. Construction of tetravalent, bispecific single-chain antibodies is taught, for example, in Coloma & Morrison, 1997, *Nat. Biotechnol.* 15, 159-63. Construction of bivalent, bispecific single-chain antibodies is taught in Mallender & Voss, 1994, *J. Biol. Chem.* 269, 199-206.

A nucleotide sequence encoding a single-chain antibody can be constructed using manual or automated nucleotide synthesis, cloned into an expression construct using standard recombinant DNA methods, and introduced into a cell to express the coding sequence, as described below. Alternatively, single-chain antibodies can be produced directly using, for example, filamentous phage technology (Verhaar *et al.*, 1995, *Int. J. Cancer* 61, 497-501; Nicholls *et al.*, 1993, *J. Immunol. Meth.* 165, 81-91).

Antibodies which specifically bind to CRIK polypeptides also can be produced by inducing *in vivo* production in the lymphocyte population or by screening immunoglobulin libraries or panels of highly specific binding reagents as disclosed in the literature (Orlandi *et al.*, *Proc. Natl. Acad. Sci.* 86, 3833-3837, 1989; Winter *et al.*, *Nature* 349, 293-299, 1991).

Other types of antibodies can be constructed and used therapeutically in methods of the invention. For example, chimeric antibodies can be constructed as disclosed in

WO 93/03151. Binding proteins which are derived from immunoglobulins and which are multivalent and multispecific, such as the "diabodies" described in WO 94/13804, also can be prepared.

5 Antibodies according to the invention can be purified by methods well known in the art. For example, antibodies can be affinity purified by passage over a column to which a CRIK polypeptide is bound. The bound antibodies can then be eluted from the column using a buffer with a high salt concentration.

10 Antisense Oligonucleotides

Antisense oligonucleotides are nucleotide sequences that are complementary to a specific DNA or RNA sequence. Once introduced into a cell, the complementary nucleotides combine with natural sequences produced by the cell to form complexes
15 and block either transcription or translation. Preferably, an antisense oligonucleotide is at least 11 nucleotides in length, but can be at least 12, 15, 20, 25, 30, 35, 40, 45, or 50 or more nucleotides long. Longer sequences also can be used. Antisense oligonucleotide molecules can be provided in a DNA construct and introduced into a cell as described above to decrease the level of CRIK gene products in the cell.

20 Antisense oligonucleotides can be deoxyribonucleotides, ribonucleotides, or a combination of both. Oligonucleotides can be synthesized manually or by an automated synthesizer, by covalently linking the 5' end of one nucleotide with the 3' end of another nucleotide with non-phosphodiester internucleotide linkages such
25 alkylphosphonates, phosphorothioates, phosphorodithioates, alkylphosphonothioates, alkylphosphonates, phosphoramidates, phosphate esters, carbamates, acetamidate, carboxymethyl esters, carbonates, and phosphate triesters. See Brown, *Meth. Mol. Biol.* 20, 1-8, 1994; Sonveaux, *Meth. Mol. Biol.* 26, 1-72, 1994; Uhlmann *et al.*, *Chem. Rev.* 90, 543-583, 1990.

30

Modifications of CRIK gene expression can be obtained by designing antisense oligonucleotides that will form duplexes to the control, 5', or regulatory regions of the CRIK gene. Oligonucleotides derived from the transcription initiation site, *e.g.*, between positions -10 and +10 from the start site, are preferred. Similarly, inhibition
5 can be achieved using "triple helix" base-pairing methodology. Triple helix pairing is useful because it causes inhibition of the ability of the double helix to open sufficiently for the binding of polymerases, transcription factors, or chaperons. Therapeutic advances using triplex DNA have been described in the literature (*e.g.*, Gee *et al.*, in Huber & Carr, MOLECULAR AND IMMUNOLOGIC APPROACHES, Futura
10 Publishing Co., Mt. Kisco, N.Y., 1994). An antisense oligonucleotide also can be designed to block translation of mRNA by preventing the transcript from binding to ribosomes.

Precise complementarity is not required for successful complex formation between
15 an antisense oligonucleotide and the complementary sequence of a CRIK polynucleotide. Antisense oligonucleotides which comprise, for example, 2, 3, 4, or 5 or more stretches of contiguous nucleotides which are precisely complementary to a CRIK polynucleotide, each separated by a stretch of contiguous nucleotides which are not complementary to adjacent CRIK nucleotides, can provide sufficient targeting
20 specificity for CRIK mRNA. Preferably, each stretch of complementary contiguous nucleotides is at least 4, 5, 6, 7, or 8 or more nucleotides in length. Non-complementary intervening sequences are preferably 1, 2, 3, or 4 nucleotides in length. One skilled in the art can easily use the calculated melting point of an antisense-sense pair to determine the degree of mismatching which will be tolerated
25 between a particular antisense oligonucleotide and a particular CRIK polynucleotide sequence.

Antisense oligonucleotides can be modified without affecting their ability to hybridize to a CRIK polynucleotide. These modifications can be internal or at one or
30 both ends of the antisense molecule. For example, internucleoside phosphate linkages can be modified by adding cholesteryl or diamine moieties with varying

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numbers of carbon residues between the amino groups and terminal ribose. Modified bases and/or sugars, such as arabinose instead of ribose, or a 3', 5'-substituted oligonucleotide in which the 3' hydroxyl group or the 5' phosphate group are substituted, also can be employed in a modified antisense oligonucleotide. These modified oligonucleotides can be prepared by methods well known in the art. *See, e.g., Agrawal et al., Trends Biotechnol. 10, 152-158, 1992; Uhlmann et al., Chem. Rev. 90, 543-584, 1990; Uhlmann et al., Tetrahedron. Lett. 215, 3539-3542, 1987.*

Ribozymes

Ribozymes are RNA molecules with catalytic activity. *See, e.g., Cech, Science 236, 1532-1539; 1987; Cech, Ann. Rev. Biochem. 59, 543-568; 1990, Cech, Curr. Opin. Struct. Biol. 2, 605-609; 1992, Couture & Stinchcomb, Trends Genet. 12, 510-515, 1996.* Ribozymes can be used to inhibit gene function by cleaving an RNA sequence, as is known in the art (*e.g., Haseloff et al., U.S. Patent 5,641,673*). The mechanism of ribozyme action involves sequence-specific hybridization of the ribozyme molecule to complementary target RNA, followed by endonucleolytic cleavage. Examples include engineered hammerhead motif ribozyme molecules that can specifically and efficiently catalyze endonucleolytic cleavage of specific nucleotide sequences.

The coding sequence of a CRIK polynucleotide can be used to generate ribozymes that will specifically bind to mRNA transcribed from the CRIK polynucleotide. Methods of designing and constructing ribozymes which can cleave other RNA molecules in trans in a highly sequence specific manner have been developed and described in the art (*see Haseloff et al. Nature 334, 585-591, 1988*). For example, the cleavage activity of ribozymes can be targeted to specific RNAs by engineering a discrete "hybridization" region into the ribozyme. The hybridization region contains a sequence complementary to the target RNA and thus specifically hybridizes with the target (*see, for example, Gerlach et al., EP 321,201*).

Specific ribozyme cleavage sites within a CRIK RNA target can be identified by scanning the target molecule for ribozyme cleavage sites which include the following sequences: GUA, GUU, and GUC. Once identified, short RNA sequences of between 15 and 20 ribonucleotides corresponding to the region of the target RNA containing the cleavage site can be evaluated for secondary structural features which may render the target inoperable. Suitability of candidate CRIK RNA targets also can be evaluated by testing accessibility to hybridization with complementary oligonucleotides using ribonuclease protection assays. Longer complementary sequences can be used to increase the affinity of the hybridization sequence for the target. The hybridizing and cleavage regions of the ribozyme can be integrally related such that upon hybridizing to the target RNA through the complementary regions, the catalytic region of the ribozyme can cleave the target.

Ribozymes can be introduced into cells as part of a DNA construct. Mechanical methods, such as microinjection, liposome-mediated transfection, electroporation, or calcium phosphate precipitation, can be used to introduce a ribozyme-containing DNA construct into cells in which it is desired to decrease CRIK expression. Alternatively, if it is desired that the cells stably retain the DNA construct, the construct can be supplied on a plasmid and maintained as a separate element or integrated into the genome of the cells, as is known in the art. A ribozyme-encoding DNA construct can include transcriptional regulatory elements, such as a promoter element, an enhancer or UAS element, and a transcriptional terminator signal, for controlling transcription of ribozymes in the cells.

As taught in Haseloff *et al.*, U.S. Patent 5,641,673, ribozymes can be engineered so that ribozyme expression will occur in response to factors that induce expression of a target gene. Ribozymes also can be engineered to provide an additional level of regulation, so that destruction of mRNA occurs only when both a ribozyme and a target gene are induced in the cells.

Differentially Expressed Genes

Described herein are methods for the identification of genes whose products interact with human CRIK. Such genes may represent genes that are differentially expressed in disorders including, but not limited to, obesity, CNS disorders, and COPD. Further, such genes may represent genes that are differentially regulated in response to manipulations relevant to the progression or treatment of such diseases. Additionally, such genes may have a temporally modulated expression, increased or decreased at different stages of tissue or organism development. A differentially expressed gene may also have its expression modulated under control versus experimental conditions. In addition, the human CRIK gene or gene product may itself be tested for differential expression.

The degree to which expression differs in a normal versus a diseased state need only be large enough to be visualized via standard characterization techniques such as differential display techniques. Other such standard characterization techniques by which expression differences may be visualized include but are not limited to, quantitative RT (reverse transcriptase), PCR, and Northern analysis.

Identification of Differentially Expressed Genes

To identify differentially expressed genes total RNA or, preferably, mRNA is isolated from tissues of interest. For example, RNA samples are obtained from tissues of experimental subjects and from corresponding tissues of control subjects. Any RNA isolation technique that does not select against the isolation of mRNA may be utilized for the purification of such RNA samples. See, for example, Ausubel *et al.*, ed., CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, Inc. New York, 1987-1993. Large numbers of tissue samples may readily be processed using techniques well known to those of skill in the art, such as, for example, the single-step RNA isolation process of Chomczynski, U.S. Patent 4,843,155.

Transcripts within the collected RNA samples that represent RNA produced by differentially expressed genes are identified by methods well known to those of skill in the art. They include, for example, differential screening (Tedder *et al.*, *Proc. Natl. Acad. Sci. U.S.A.* 85, 208-12, 1988), subtractive hybridization (Hedrick *et al.*, *Nature* 308, 149-53; Lee *et al.*, *Proc. Natl. Acad. Sci. U.S.A.* 88, 2825, 1984), and, preferably, differential display (Liang & Pardee, *Science* 257, 967-71, 1992; U.S. Patent 5,262,311).

The differential expression information may itself suggest relevant methods for the treatment of disorders involving the human CRIK. For example, treatment may include a modulation of expression of the differentially expressed genes and/or the gene encoding the human CRIK. The differential expression information may indicate whether the expression or activity of the differentially expressed gene or gene product or the human CRIK gene or gene product are up-regulated or down-regulated.

Screening Methods

The invention provides assays for screening test compounds that bind to or modulate the activity of a CRIK polypeptide or a CRIK polynucleotide. A test compound preferably binds to a CRIK polypeptide or polynucleotide. More preferably, a test compound decreases or increases enzymatic activity by at least about 10, preferably about 50, more preferably about 75, 90, or 100% relative to the absence of the test compound.

Test Compounds

Test compounds can be pharmacologic agents already known in the art or can be compounds previously unknown to have any pharmacological activity. The compounds can be naturally occurring or designed in the laboratory. They can be isolated from microorganisms, animals, or plants, and can be produced

recombinantly, or synthesized by chemical methods known in the art. If desired, test compounds can be obtained using any of the numerous combinatorial library methods known in the art, including but not limited to, biological libraries, spatially addressable parallel solid phase or solution phase libraries, synthetic library methods requiring deconvolution, the "one-bead one-compound" library method, and synthetic library methods using affinity chromatography selection. The biological library approach is limited to polypeptide libraries, while the other four approaches are applicable to polypeptide, non-peptide oligomer, or small molecule libraries of compounds. See Lam, *Anticancer Drug Des.* 12, 145, 1997.

Methods for the synthesis of molecular libraries are well known in the art (see, for example, DeWitt *et al.*, *Proc. Natl. Acad. Sci. U.S.A.* 90, 6909, 1993; Erb *et al.* *Proc. Natl. Acad. Sci. U.S.A.* 91, 11422, 1994; Zuckermann *et al.*, *J. Med. Chem.* 37, 2678, 1994; Cho *et al.*, *Science* 261, 1303, 1993; Carell *et al.*, *Angew. Chem. Int. Ed. Engl.* 33, 2059, 1994; Carell *et al.*, *Angew. Chem. Int. Ed. Engl.* 33, 2061; Gallop *et al.*, *J. Med. Chem.* 37, 1233, 1994). Libraries of compounds can be presented in solution (see, e.g., Houghten, *BioTechniques* 13, 412-421, 1992), or on beads (Lam, *Nature* 354, 82-84, 1991), chips (Fodor, *Nature* 364, 555-556, 1993), bacteria or spores (Ladner, U.S. Patent 5,223,409), plasmids (Cull *et al.*, *Proc. Natl. Acad. Sci. U.S.A.* 89, 1865-1869, 1992), or phage (Scott & Smith, *Science* 249, 386-390, 1990; Devlin, *Science* 249, 404-406, 1990); Cwirla *et al.*, *Proc. Natl. Acad. Sci.* 97, 6378-6382, 1990; Felici, *J. Mol. Biol.* 222, 301-310, 1991; and Ladner, U.S. Patent 5,223,409).

High Throughput Screening

Test compounds can be screened for the ability to bind to CRIK polypeptides or polynucleotides or to affect CRIK activity or CRIK gene expression using high throughput screening. Using high throughput screening, many discrete compounds can be tested in parallel so that large numbers of test compounds can be quickly screened. The most widely established techniques utilize 96-well microtiter plates. The wells of the microtiter plates typically require assay volumes that range from 50

to 500 μ l. In addition to the plates, many instruments, materials, pipettors, robotics, plate washers, and plate readers are commercially available to fit the 96-well format.

Alternatively, "free format assays," or assays that have no physical barrier between
5 samples, can be used. For example, an assay using pigment cells (melanocytes) in a simple homogeneous assay for combinatorial peptide libraries is described by Jayawickreme *et al.*, *Proc. Natl. Acad. Sci. U.S.A.* 19, 1614-18 (1994). The cells are placed under agarose in petri dishes, then beads that carry combinatorial compounds are placed on the surface of the agarose. The combinatorial compounds are partially
10 released the compounds from the beads. Active compounds can be visualized as dark pigment areas because, as the compounds diffuse locally into the gel matrix, the active compounds cause the cells to change colors.

Another example of a free format assay is described by Chelsky, "Strategies for
15 Screening Combinatorial Libraries: Novel and Traditional Approaches," reported at the First Annual Conference of The Society for Biomolecular Screening in Philadelphia, Pa. (Nov. 7-10, 1995). Chelsky placed a simple homogenous enzyme assay for carbonic anhydrase inside an agarose gel such that the enzyme in the gel would cause a color change throughout the gel. Thereafter, beads carrying
20 combinatorial compounds via a photolinker were placed inside the gel and the compounds were partially released by UV-light. Compounds that inhibited the enzyme were observed as local zones of inhibition having less color change.

Yet another example is described by Salmon *et al.*, *Molecular Diversity* 2, 57-63
25 (1996). In this example, combinatorial libraries were screened for compounds that had cytotoxic effects on cancer cells growing in agar.

Another high throughput screening method is described in Beutel *et al.*, U.S. Patent 5,976,813. In this method, test samples are placed in a porous matrix. One or more
30 assay components are then placed within, on top of, or at the bottom of a matrix such as a gel, a plastic sheet, a filter, or other form of easily manipulated solid support.

When samples are introduced to the porous matrix they diffuse sufficiently slowly, such that the assays can be performed without the test samples running together.

Binding Assays

5

For binding assays, the test compound is preferably a small molecule that binds to and occupies, for example, the active site of the CRIK polypeptide, such that normal biological activity is prevented. Examples of such small molecules include, but are not limited to, small peptides or peptide-like molecules.

10

In binding assays, either the test compound or the CRIK polypeptide can comprise a detectable label, such as a fluorescent, radioisotopic, chemiluminescent, or enzymatic label, such as horseradish peroxidase, alkaline phosphatase, or luciferase. Detection of a test compound that is bound to the CRIK polypeptide can then be accomplished, for example, by direct counting of radioemmission, by scintillation counting, or by determining conversion of an appropriate substrate to a detectable product.

15

20

Alternatively, binding of a test compound to a CRIK polypeptide can be determined without labeling either of the interactants. For example, a microphysiometer can be used to detect binding of a test compound with a CRIK polypeptide. A microphysiometer (*e.g.*, Cytosensor™) is an analytical instrument that measures the rate at which a cell acidifies its environment using a light-addressable potentiometric sensor (LAPS). Changes in this acidification rate can be used as an indicator of the interaction between a test compound and a CRIK polypeptide (McConnell *et al.*, *Science* 257, 1906-1912, 1992).

25

30

Determining the ability of a test compound to bind to a CRIK polypeptide also can be accomplished using a technology such as real-time Bimolecular Interaction Analysis (BIA) (Sjolander & Urbaniczky, *Anal. Chem.* 63, 2338-2345, 1991, and Szabo *et al.*, *Curr. Opin. Struct. Biol.* 5, 699-705, 1995). BIA is a technology for studying biospecific interactions in real time, without labeling any of the interactants

(e.g., BIAcoreTM). Changes in the optical phenomenon surface plasmon resonance (SPR) can be used as an indication of real-time reactions between biological molecules.

5 In yet another aspect of the invention, a CRIK polypeptide can be used as a “bait protein” in a two-hybrid assay or three-hybrid assay (see, e.g., U.S. Patent 5,283,317; Zervos *et al.*, *Cell* 72, 223-232, 1993; Madura *et al.*, *J. Biol. Chem.* 268, 12046-12054, 1993; Bartel *et al.*, *BioTechniques* 14, 920-924, 1993; Iwabuchi *et al.*, *Oncogene* 8, 1693-1696, 1993; and Brent W094/10300), to identify other proteins
10 which bind to or interact with the CRIK polypeptide and modulate its activity.

The two-hybrid system is based on the modular nature of most transcription factors, which consist of separable DNA-binding and activation domains. Briefly, the assay utilizes two different DNA constructs. For example, in one construct, polynucleotide
15 encoding a CRIK polypeptide can be fused to a polynucleotide encoding the DNA binding domain of a known transcription factor (e.g., GAL-4). In the other construct a DNA sequence that encodes an unidentified protein (“prey” or “sample”) can be fused to a polynucleotide that codes for the activation domain of the known transcription factor. If the “bait” and the “prey” proteins are able to interact *in vivo*
20 to form an protein-dependent complex, the DNA-binding and activation domains of the transcription factor are brought into close proximity. This proximity allows transcription of a reporter gene (e.g., LacZ), which is operably linked to a transcriptional regulatory site responsive to the transcription factor. Expression of the reporter gene can be detected, and cell colonies containing the functional
25 transcription factor can be isolated and used to obtain the DNA sequence encoding the protein that interacts with the CRIK polypeptide.

It may be desirable to immobilize either the CRIK polypeptide (or polynucleotide) or the test compound to facilitate separation of bound from unbound forms of one or
30 both of the interactants, as well as to accommodate automation of the assay. Thus, either the CRIK polypeptide (or polynucleotide) or the test compound can be bound

to a solid support. Suitable solid supports include, but are not limited to, glass or plastic slides, tissue culture plates, microtiter wells, tubes, silicon chips, or particles such as beads (including, but not limited to, latex, polystyrene, or glass beads). Any method known in the art can be used to attach the enzyme polypeptide (or polynucleotide) or test compound to a solid support, including use of covalent and non-covalent linkages, passive absorption, or pairs of binding moieties attached respectively to the polypeptide (or polynucleotide) or test compound and the solid support. Test compounds are preferably bound to the solid support in an array, so that the location of individual test compounds can be tracked. Binding of a test compound to a CRIK polypeptide (or polynucleotide) can be accomplished in any vessel suitable for containing the reactants. Examples of such vessels include microtiter plates, test tubes, and microcentrifuge tubes.

In one embodiment, the CRIK polypeptide is a fusion protein comprising a domain that allows the CRIK polypeptide to be bound to a solid support. For example, glutathione-S-transferase fusion proteins can be adsorbed onto glutathione sepharose beads (Sigma Chemical, St. Louis, Mo.) or glutathione derivatized microtiter plates, which are then combined with the test compound or the test compound and the non-adsorbed CRIK polypeptide; the mixture is then incubated under conditions conducive to complex formation (*e.g.*, at physiological conditions for salt and pH). Following incubation, the beads or microtiter plate wells are washed to remove any unbound components. Binding of the interactants can be determined either directly or indirectly, as described above. Alternatively, the complexes can be dissociated from the solid support before binding is determined.

Other techniques for immobilizing proteins or polynucleotides on a solid support also can be used in the screening assays of the invention. For example, either a CRIK polypeptide (or polynucleotide) or a test compound can be immobilized utilizing conjugation of biotin and streptavidin. Biotinylated CRIK polypeptides (or polynucleotides) or test compounds can be prepared from biotin-NHS(N-hydroxy-succinimide) using techniques well known in the art (*e.g.*, biotinylation kit, Pierce

Chemicals, Rockford, Ill.) and immobilized in the wells of streptavidin-coated 96 well plates (Pierce Chemical). Alternatively, antibodies which specifically bind to a CRIK polypeptide, polynucleotide, or a test compound, but which do not interfere with a desired binding site, such as the active site of the CRIK polypeptide, can be derivatized to the wells of the plate. Unbound target or protein can be trapped in the wells by antibody conjugation.

Methods for detecting such complexes, in addition to those described above for the GST-immobilized complexes, include immunodetection of complexes using antibodies which specifically bind to the CRIK polypeptide or test compound, enzyme-linked assays which rely on detecting an activity of the CRIK polypeptide, and SDS gel electrophoresis under non-reducing conditions.

Screening for test compounds which bind to a CRIK polypeptide or polynucleotide also can be carried out in an intact cell. Any cell which comprises a CRIK polypeptide or polynucleotide can be used in a cell-based assay system. A CRIK polynucleotide can be naturally occurring in the cell or can be introduced using techniques such as those described above. Binding of the test compound to a CRIK polypeptide or polynucleotide is determined as described above.

Enzyme Assays

Test compounds can be tested for the ability to increase or decrease the enzymatic activity of a human CRIK polypeptide. Enzymatic activity can be measured, for example, as described in Di Cunto *et al.*, J Biol Chem. 1998 Nov 6;273(45):29706-11.

Enzyme assays can be carried out after contacting either a purified CRIK polypeptide, a cell membrane preparation, or an intact cell with a test compound. A test compound that decreases an enzymatic activity of a CRIK polypeptide by at least about 10, preferably about 50, more preferably about 75, 90, or 100% is identified as

a potential therapeutic agent for decreasing CRIK activity. A test compound which increases an enzymatic activity of a human CRIK polypeptide by at least about 10, preferably about 50, more preferably about 75, 90, or 100% is identified as a potential therapeutic agent for increasing human CRIK activity.

5

Gene Expression

In another embodiment, test compounds that increase or decrease CRIK gene expression are identified. A CRIK polynucleotide is contacted with a test compound, and the expression of an RNA or polypeptide product of the CRIK polynucleotide is determined. The level of expression of appropriate mRNA or polypeptide in the presence of the test compound is compared to the level of expression of mRNA or polypeptide in the absence of the test compound. The test compound can then be identified as a modulator of expression based on this comparison. For example, when expression of mRNA or polypeptide is greater in the presence of the test compound than in its absence, the test compound is identified as a stimulator or enhancer of the mRNA or polypeptide expression. Alternatively, when expression of the mRNA or polypeptide is less in the presence of the test compound than in its absence, the test compound is identified as an inhibitor of the mRNA or polypeptide expression.

20

The level of CRIK mRNA or polypeptide expression in the cells can be determined by methods well known in the art for detecting mRNA or polypeptide. Either qualitative or quantitative methods can be used. The presence of polypeptide products of a CRIK polynucleotide can be determined, for example, using a variety of techniques known in the art, including immunochemical methods such as radioimmunoassay, Western blotting, and immunohistochemistry. Alternatively, polypeptide synthesis can be determined *in vivo*, in a cell culture, or in an *in vitro* translation system by detecting incorporation of labeled amino acids into a CRIK polypeptide.

30

Such screening can be carried out either in a cell-free assay system or in an intact cell. Any cell that expresses a CRIK polynucleotide can be used in a cell-based assay system. The CRIK polynucleotide can be naturally occurring in the cell or can be introduced using techniques such as those described above. Either a primary
5 culture or an established cell line, such as CHO or human embryonic kidney 293 cells, can be used.

Pharmaceutical Compositions

10 The invention also provides pharmaceutical compositions that can be administered to a patient to achieve a therapeutic effect. Pharmaceutical compositions of the invention can comprise, for example, a CRIK polypeptide, CRIK polynucleotide, ribozymes or antisense oligonucleotides, antibodies which specifically bind to a CRIK polypeptide, or mimetics, activators, or inhibitors of a CRIK polypeptide
15 activity. The compositions can be administered alone or in combination with at least one other agent, such as stabilizing compound, which can be administered in any sterile, biocompatible pharmaceutical carrier, including, but not limited to, saline, buffered saline, dextrose, and water. The compositions can be administered to a patient alone, or in combination with other agents, drugs or hormones.

20 In addition to the active ingredients, these pharmaceutical compositions can contain suitable pharmaceutically-acceptable carriers comprising excipients and auxiliaries that facilitate processing of the active compounds into preparations which can be used pharmaceutically. Pharmaceutical compositions of the invention can be
25 administered by any number of routes including, but not limited to, oral, intravenous, intramuscular, intra-arterial, intramedullary, intrathecal, intraventricular, transdermal, subcutaneous, intraperitoneal, intranasal, parenteral, topical, sublingual, or rectal means. Pharmaceutical compositions for oral administration can be formulated using pharmaceutically acceptable carriers well known in the art in dosages suitable for
30 oral administration. Such carriers enable the pharmaceutical compositions to be

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formulated as tablets, pills, dragees, capsules, liquids, gels, syrups, slurries, suspensions, and the like, for ingestion by the patient.

- 5 Pharmaceutical preparations for oral use can be obtained through combination of active compounds with solid excipient, optionally grinding a resulting mixture, and processing the mixture of granules, after adding suitable auxiliaries, if desired, to obtain tablets or dragee cores. Suitable excipients are carbohydrate or protein fillers, such as sugars, including lactose, sucrose, mannitol, or sorbitol; starch from corn, wheat, rice, potato, or other plants; cellulose, such as methyl cellulose, hydroxypropylmethyl-cellulose, or sodium carboxymethylcellulose; gums including arabic and tragacanth; and proteins such as gelatin and collagen. If desired, disintegrating or solubilizing agents can be added, such as the cross-linked polyvinyl pyrrolidone, agar, alginic acid, or a salt thereof, such as sodium alginate.
- 10
- 15 Dragee cores can be used in conjunction with suitable coatings, such as concentrated sugar solutions, which also can contain gum arabic, talc, polyvinylpyrrolidone, carbopol gel, polyethylene glycol, and/or titanium dioxide, lacquer solutions, and suitable organic solvents or solvent mixtures. Dyestuffs or pigments can be added to the tablets or dragee coatings for product identification or to characterize the quantity of active compound, *i.e.*, dosage.
- 20

- Pharmaceutical preparations that can be used orally include push-fit capsules made of gelatin, as well as soft, sealed capsules made of gelatin and a coating, such as glycerol or sorbitol. Push-fit capsules can contain active ingredients mixed with a filler or binders, such as lactose or starches, lubricants, such as talc or magnesium stearate, and, optionally, stabilizers. In soft capsules, the active compounds can be dissolved or suspended in suitable liquids, such as fatty oils, liquid, or liquid polyethylene glycol with or without stabilizers.
- 25

- 30 Pharmaceutical formulations suitable for parenteral administration can be formulated in aqueous solutions, preferably in physiologically compatible buffers such as

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Hanks' solution, Ringer's solution, or physiologically buffered saline. Aqueous injection suspensions can contain substances that increase the viscosity of the suspension, such as sodium carboxymethyl cellulose, sorbitol, or dextran. Additionally, suspensions of the active compounds can be prepared as appropriate oily injection suspensions. Suitable lipophilic solvents or vehicles include fatty oils such as sesame oil, or synthetic fatty acid esters, such as ethyl oleate or triglycerides, or liposomes. Non-lipid polycationic amino polymers also can be used for delivery. Optionally, the suspension also can contain suitable stabilizers or agents that increase the solubility of the compounds to allow for the preparation of highly concentrated solutions. For topical or nasal administration, penetrants appropriate to the particular barrier to be permeated are used in the formulation. Such penetrants are generally known in the art.

The pharmaceutical compositions of the present invention can be manufactured in a manner that is known in the art, *e.g.*, by means of conventional mixing, dissolving, granulating, dragee-making, levigating, emulsifying, encapsulating, entrapping, or lyophilizing processes. The pharmaceutical composition can be provided as a salt and can be formed with many acids, including but not limited to, hydrochloric, sulfuric, acetic, lactic, tartaric, malic, succinic, etc. Salts tend to be more soluble in aqueous or other protonic solvents than are the corresponding free base forms. In other cases, the preferred preparation can be a lyophilized powder which can contain any or all of the following: 1-50 mM histidine, 0.1%-2% sucrose, and 2-7% mannitol, at a pH range of 4.5 to 5.5, that is combined with buffer prior to use.

Further details on techniques for formulation and administration can be found in the latest edition of REMINGTON'S PHARMACEUTICAL SCIENCES (Maack Publishing Co., Easton, Pa.). After pharmaceutical compositions have been prepared, they can be placed in an appropriate container and labeled for treatment of an indicated condition. Such labeling would include amount, frequency, and method of administration.

Therapeutic Indications and Methods

Human CRIK can be regulated to treat obesity, CNS disorders, and COPD.

5 Obesity. Obesity and overweight are defined as an excess of body fat relative to lean
body mass. An increase in caloric intake or a decrease in energy expenditure or both
can bring about this imbalance leading to surplus energy being stored as fat. Obesity
is associated with important medical morbidities and an increase in mortality. The
causes of obesity are poorly understood and may be due to genetic factors,
10 environmental factors or a combination of the two to cause a positive energy balance.
In contrast, anorexia and cachexia are characterized by an imbalance in energy intake
versus energy expenditure leading to a negative energy balance and weight loss.
Agents that either increase energy expenditure and/or decrease energy intake,
absorption or storage would be useful for treating obesity, overweight, and associated
15 comorbidities. Agents that either increase energy intake and/or decrease energy
expenditure or increase the amount of lean tissue would be useful for treating
cachexia, anorexia and wasting disorders.

This gene, translated proteins and agents which modulate this gene or portions of the
20 gene or its products are useful for treating obesity, overweight, anorexia, cachexia,
wasting disorders, appetite suppression, appetite enhancement, increases or decreases
in satiety, modulation of body weight, and/or other eating disorders such as bulimia.
Also this gene, translated proteins and agents which modulate this gene or portions of
the gene or its products are useful for treating obesity/overweight-associated
25 comorbidities including hypertension, type 2 diabetes, coronary artery disease,
hyperlipidemia, stroke, gallbladder disease, gout, osteoarthritis, sleep apnea and
respiratory problems, some types of cancer including endometrial, breast, prostate,
and colon cancer, thrombotic disease, polycystic ovarian syndrome, reduced fertility,
complications of pregnancy, menstrual irregularities, hirsutism, stress incontinence,
30 and depression.

The hypothalamus has been considered as the feeding control center. Many neuro-peptides, hormones, neurotransmitters, etc. that play important roles in the control of energy homeostasis have been identified in the hypothalamus. See *J. Lip. Res.* 40, 1735-46, 1999; *Pharm. Rev.* 52, 35-61, 2000. Leptin signaling pathway, MC4, and 5-HT_{2C} systems in the hypothalamus play critical roles in the control of body weight homeostasis. Therefore, a gene selectively expressed in the hypothalamus, such as the human CRIK of the invention, is a potential obesity target.

CNS disorders. Central and peripheral nervous system disorders also can be treated, such as primary and secondary disorders after brain injury, disorders of mood, anxiety disorders, disorders of thought and volition, disorders of sleep and wakefulness, diseases of the motor unit, such as neurogenic and myopathic disorders, neurodegenerative disorders such as Alzheimer's and Parkinson's disease, and processes of peripheral and chronic pain. Pain that is associated with CNS disorders also can be treated by regulating the activity of human CRIK. Pain which can be treated includes that associated with central nervous system disorders, such as multiple sclerosis, spinal cord injury, sciatica, failed back surgery syndrome, traumatic brain injury, epilepsy, Parkinson's disease, post-stroke, and vascular lesions in the brain and spinal cord (*e.g.*, infarct, hemorrhage, vascular malformation). Non-central neuropathic pain includes that associated with post mastectomy pain, reflex sympathetic dystrophy (RSD), trigeminal neuralgia-radioculopathy, post-surgical pain, HIV/AIDS related pain, cancer pain, metabolic neuropathies (*e.g.*, diabetic neuropathy, vasculitic neuropathy secondary to connective tissue disease), paraneoplastic polyneuropathy associated, for example, with carcinoma of lung, or leukemia, or lymphoma, or carcinoma of prostate, colon or stomach, trigeminal neuralgia, cranial neuralgias, and post-herpetic neuralgia. Pain associated with cancer and cancer treatment also can be treated, as can headache pain (for example, migraine with aura, migraine without aura, and other migraine disorders), episodic and chronic tension-type headache, tension-type like headache, cluster headache, and chronic paroxysmal hemicrania.

COPD. Chronic obstructive pulmonary (or airways) disease (COPD) is a condition defined physiologically as airflow obstruction that generally results from a mixture of emphysema and peripheral airway obstruction due to chronic bronchitis (Senior & Shapiro, *Pulmonary Diseases and Disorders*, 3d ed., New York, McGraw-Hill, 1998, pp. 659-681, 1998; Barnes, *Chest* 117, 10S-14S, 2000). Emphysema is characterized by destruction of alveolar walls leading to abnormal enlargement of the air spaces of the lung. Chronic bronchitis is defined clinically as the presence of chronic productive cough for three months in each of two successive years. In COPD, airflow obstruction is usually progressive and is only partially reversible. By far the most important risk factor for development of COPD is cigarette smoking, although the disease does occur in non-smokers.

Chronic inflammation of the airways is a key pathological feature of COPD (Senior & Shapiro, 1998). The inflammatory cell population comprises increased numbers of macrophages, neutrophils, and CD8⁺ lymphocytes. Inhaled irritants, such as cigarette smoke, activate macrophages which are resident in the respiratory tract, as well as epithelial cells leading to release of chemokines (*e.g.*, interleukin-8) and other chemotactic factors. These chemotactic factors act to increase the neutrophil/monocyte trafficking from the blood into the lung tissue and airways. Neutrophils and monocytes recruited into the airways can release a variety of potentially damaging mediators such as proteolytic enzymes and reactive oxygen species. Matrix degradation and emphysema, along with airway wall thickening, surfactant dysfunction, and mucus hypersecretion, all are potential sequelae of this inflammatory response that lead to impaired airflow and gas exchange.

Protein kinases are signal transducing enzymes that phosphorylate proteins, including other kinases, and, along with protein phosphatases, regulate the level and extent of protein phosphorylation and activation. Intracellular signalling pathways have important roles in inflammatory processes. These pathways may be activated by cytokines, oxidant stress and other inflammatory mediators (reviewed in Kyraikis and Avruch, 1996 and 2001). For example, the pro-inflammatory cytokines, tumor

necrosis factor α (TNF α) and interleukin-1 activate the protein ser/thr kinases c-Jun-NH2-terminal kinase (JNK) and p38 mitogen-activated protein (MAP) kinase, leading to activation of AP-1 and IKB kinase (IKK), which, in turn, leads to activation of the transcription factor NF κ B. Activation of NF κ B is required for the transcription of several pro-inflammatory molecules, including interleukin-8 and ICAM-1. Enzymes of the MAP kinase class may also act to increase cytokine production by stabilization of mRNA (Winzen et al., 1999).

Inhibition of specific protein kinases has been shown to elicit anti-inflammatory effects. For example, the accumulation of polymorphonuclear leukocytes in murine lung following intratracheal administration of bacterial lipopolysaccharide can be blocked by inhibition of p38 MAP kinase (Nick, et al. 2000). As a further example, aerosol delivery to rat lungs of antisense oligodeoxynucleotides to syk kinase mRNA, suppressed nitric oxide and TNF α production from alveolar macrophages stimulated with IgG-anti-IgG complexes (Stenton et al. 2000). Protein kinase subtypes are therefore attractive therapeutic targets for the attenuation of the inflammatory response in COPD. See Kyriakis, J.M. and Avruch J. Sounding the alarm: protein kinase cascades activated by stress and inflammation. *J Biol Chem* 1996, **271**:24313-6; Kyriakis, J.M. and Avruch, J. Mammalian mitogen-activated protein kinase signal transduction pathways activated by stress and inflammation. *J. Physiol. Rev.* 2001, **81**:807-69; Winzen, R., Kracht, M., Ritter, B., Wilhelm, A., Chen C.A., Shyu, A., Müller, M., Gaestel, M., Resch, K., and Holtmann, H. The p38 MAP kinase pathway signals for cytokine-induced mRNA stabilization via MAP kinase-activated protein kinase 2 and an AU-rich region-targeted mechanism. *EMBO J.* 1999, **18**: 4969-4980; Nick, J.A., Young, S.K., Brown, K.K., Avdi, N.J., Arndt, P.G., Suratt, B.T., Janes, M.S., Henson, P.M., Worthen, G.S. Role of p38 mitogen-activated protein kinase in a murine model of pulmonary inflammation. *J Immunol.* 2000, **164**:2151-9; and Stenton, G.R., Kim, M.K., Nohara, O., Chen, C.F., Hirji, N., Wills, F.L., Gilchrist, M., Hwang, P.H., Park, J.G., Finlay, W., Jones, R.L., Befus, A.D., Schreiber, A.D. Aerosolized Syk antisense suppresses Syk expression,

mediator release from macrophages, and pulmonary inflammation. J Immunol 2000, 164:3790-7.

5 This invention further pertains to the use of novel agents identified by the screening assays described above. Accordingly, it is within the scope of this invention to use a test compound identified as described herein in an appropriate animal model. For example, an agent identified as described herein (*e.g.*, a modulating agent, an antisense nucleic acid molecule, a specific antibody, ribozyme, or a CRIK polypeptide binding molecule) can be used in an animal model to determine the efficacy, toxicity, or side effects of treatment with such an agent. Alternatively, an agent identified as described herein can be used in an animal model to determine the mechanism of action of such an agent. Furthermore, this invention pertains to uses of novel agents identified by the above-described screening assays for treatments as described herein.

15 A reagent which affects CRIK activity can be administered to a human cell, either *in vitro* or *in vivo*, to reduce CRIK activity. The reagent preferably binds to an expression product of a human CRIK gene. If the expression product is a protein, the reagent is preferably an antibody. For treatment of human cells *ex vivo*, an antibody can be added to a preparation of stem cells that have been removed from the body. The cells can then be replaced in the same or another human body, with or without clonal propagation, as is known in the art.

25 In one embodiment, the reagent is delivered using a liposome. Preferably, the liposome is stable in the animal into which it has been administered for at least about 30 minutes, more preferably for at least about 1 hour, and even more preferably for at least about 24 hours. A liposome comprises a lipid composition that is capable of targeting a reagent, particularly a polynucleotide, to a particular site in an animal, such as a human. Preferably, the lipid composition of the liposome is capable of targeting to a specific organ of an animal, such as the lung, liver, spleen, heart brain, lymph nodes, and skin.

A liposome useful in the present invention comprises a lipid composition that is capable of fusing with the plasma membrane of the targeted cell to deliver its contents to the cell. Preferably, the transfection efficiency of a liposome is about
5 0.5 μg of DNA per 16 nmole of liposome delivered to about 10^6 cells, more preferably about 1.0 μg of DNA per 16 nmole of liposome delivered to about 10^6 cells, and even more preferably about 2.0 μg of DNA per 16 nmol of liposome delivered to about 10^6 cells. Preferably, a liposome is between about 100 and 500 nm, more preferably between about 150 and 450 nm, and even more preferably
10 between about 200 and 400 nm in diameter.

Suitable liposomes for use in the present invention include those liposomes standardly used in, for example, gene delivery methods known to those of skill in the art. More preferred liposomes include liposomes having a polycationic lipid
15 composition and/or liposomes having a cholesterol backbone conjugated to polyethylene glycol. Optionally, a liposome comprises a compound capable of targeting the liposome to a particular cell type, such as a cell-specific ligand exposed on the outer surface of the liposome.

20 Complexing a liposome with a reagent such as an antisense oligonucleotide or ribozyme can be achieved using methods that are standard in the art (see, for example, U.S. Patent 5,705,151). Preferably, from about 0.1 μg to about 10 μg of polynucleotide is combined with about 8 nmol of liposomes, more preferably from about 0.5 μg to about 5 μg of polynucleotides are combined with about 8 nmol lipo-
25 somes, and even more preferably about 1.0 μg of polynucleotides is combined with about 8 nmol liposomes.

In another embodiment, antibodies can be delivered to specific tissues *in vivo* using receptor-mediated targeted delivery. Receptor-mediated DNA delivery techniques
30 are taught in, for example, Findeis *et al.* *Trends in Biotechnol.* 11, 202-05 (1993); Chiou *et al.*, GENE THERAPEUTICS: METHODS AND APPLICATIONS OF DIRECT GENE

TRANSFER (J.A. Wolff, ed.) (1994); Wu & Wu, *J. Biol. Chem.* 263, 621-24 (1988); Wu *et al.*, *J. Biol. Chem.* 269, 542-46 (1994); Zenke *et al.*, *Proc. Natl. Acad. Sci. U.S.A.* 87, 3655-59 (1990); Wu *et al.*, *J. Biol. Chem.* 266, 338-42 (1991).

5 Determination of a Therapeutically Effective Dose

The determination of a therapeutically effective dose is well within the capability of those skilled in the art. A therapeutically effective dose refers to that amount of active ingredient which increases or decreases CRIK activity relative to the CRIK activity which occurs in the absence of the therapeutically effective dose.

For any compound, the therapeutically effective dose can be estimated initially either in cell culture assays or in animal models, usually mice, rabbits, dogs, or pigs. The animal model also can be used to determine the appropriate concentration range and route of administration. Such information can then be used to determine useful doses and routes for administration in humans.

Therapeutic efficacy and toxicity, *e.g.*, ED₅₀ (the dose therapeutically effective in 50% of the population) and LD₅₀ (the dose lethal to 50% of the population), can be determined by standard pharmaceutical procedures in cell cultures or experimental animals. The dose ratio of toxic to therapeutic effects is the therapeutic index, and it can be expressed as the ratio, LD₅₀/ED₅₀.

Pharmaceutical compositions that exhibit large therapeutic indices are preferred. The data obtained from cell culture assays and animal studies is used in formulating a range of dosage for human use. The dosage contained in such compositions is preferably within a range of circulating concentrations that include the ED₅₀ with little or no toxicity. The dosage varies within this range depending upon the dosage form employed, sensitivity of the patient, and the route of administration.

The exact dosage will be determined by the practitioner, in light of factors related to the subject that requires treatment. Dosage and administration are adjusted to provide sufficient levels of the active ingredient or to maintain the desired effect. Factors that can be taken into account include the severity of the disease state, general health of the subject, age, weight, and gender of the subject, diet, time and frequency of administration, drug combination(s), reaction sensitivities, and tolerance/response to therapy. Long-acting pharmaceutical compositions can be administered every 3 to 4 days, every week, or once every two weeks depending on the half-life and clearance rate of the particular formulation.

Normal dosage amounts can vary from 0.1 to 100,000 micrograms, up to a total dose of about 1 g, depending upon the route of administration. Guidance as to particular dosages and methods of delivery is provided in the literature and generally available to practitioners in the art. Those skilled in the art will employ different formulations for nucleotides than for proteins or their inhibitors. Similarly, delivery of polynucleotides or polypeptides will be specific to particular cells, conditions, locations, etc.

If the reagent is a single-chain antibody, polynucleotides encoding the antibody can be constructed and introduced into a cell either *ex vivo* or *in vivo* using well-established techniques including, but not limited to, transferrin-polycation-mediated DNA transfer, transfection with naked or encapsulated nucleic acids, liposome-mediated cellular fusion, intracellular transportation of DNA-coated latex beads, protoplast fusion, viral infection, electroporation, "gene gun," and DEAE- or calcium phosphate-mediated transfection.

Effective *in vivo* dosages of an antibody are in the range of about 5 µg to about 50 µg/kg, about 50 µg to about 5 mg/kg, about 100 µg to about 500 µg/kg of patient body weight, and about 200 to about 250 µg/kg of patient body weight. For administration of polynucleotides encoding single-chain antibodies, effective *in vivo* dosages are in the range of about 100 ng to about 200 ng, 500 ng to about 50 mg,

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about 1 μ g to about 2 mg, about 5 μ g to about 500 μ g, and about 20 μ g to about 100 μ g of DNA.

5 If the expression product is mRNA, the reagent is preferably an antisense oligonucleotide or a ribozyme. Polynucleotides that express antisense oligonucleotides or ribozymes can be introduced into cells by a variety of methods, as described above.

10 Preferably, a reagent reduces expression of a CRIK gene or the activity of a CRIK polypeptide by at least about 10, preferably about 50, more preferably about 75, 90, or 100% relative to the absence of the reagent. The effectiveness of the mechanism chosen to decrease the level of expression of a CRIK gene or the activity of a CRIK polypeptide can be assessed using methods well known in the art, such as hybridization of nucleotide probes to CRIK-specific mRNA, quantitative RT-PCR, immunologic detection of a CRIK polypeptide, or measurement of CRIK activity.

15 In any of the embodiments described above, any of the pharmaceutical compositions of the invention can be administered in combination with other appropriate therapeutic agents. *Selection of the appropriate agents for use in combination* therapy can be made by one of ordinary skill in the art, according to conventional pharmaceutical principles. The combination of therapeutic agents can act synergistically to effect the treatment or prevention of the various disorders described above. Using this approach, one may be able to achieve therapeutic efficacy with lower dosages of each agent, thus reducing the potential for adverse side effects.

25 Any of the therapeutic methods described above can be applied to any subject in need of such therapy, including, for example, mammals such as dogs, cats, cows, horses, rabbits, monkeys, and most preferably, humans.

Diagnostic Methods

Human CRIK also can be used in diagnostic assays for detecting diseases and abnormalities or susceptibility to diseases and abnormalities related to the presence of mutations in the nucleic acid sequences that encode the enzyme. For example, differences can be determined between the cDNA or genomic sequence encoding CRIK in individuals afflicted with a disease and in normal individuals. If a mutation is observed in some or all of the afflicted individuals but not in normal individuals, then the mutation is likely to be the causative agent of the disease.

Sequence differences between a reference gene and a gene having mutations can be revealed by the direct DNA sequencing method. In addition, cloned DNA segments can be employed as probes to detect specific DNA segments. The sensitivity of this method is greatly enhanced when combined with PCR. For example, a sequencing primer can be used with a double-stranded PCR product or a single-stranded template molecule generated by a modified PCR. The sequence determination is performed by conventional procedures using radiolabeled nucleotides or by automatic sequencing procedures using fluorescent tags.

Genetic testing based on DNA sequence differences can be carried out by detection of alteration in electrophoretic mobility of DNA fragments in gels with or without denaturing agents. Small sequence deletions and insertions can be visualized, for example, by high resolution gel electrophoresis. DNA fragments of different sequences can be distinguished on denaturing formamide gradient gels in which the mobilities of different DNA fragments are retarded in the gel at different positions according to their specific melting or partial melting temperatures (*see, e.g., Myers et al., Science 230, 1242, 1985*). Sequence changes at specific locations can also be revealed by nuclease protection assays, such as RNase and S 1 protection or the chemical cleavage method (*e.g., Cotton et al., Proc. Natl. Acad. Sci. USA 85, 4397-4401, 1985*). Thus, the detection of a specific DNA sequence can be performed by methods such as hybridization, RNase protection, chemical cleavage, direct DNA

sequencing or the use of restriction enzymes and Southern blotting of genomic DNA. In addition to direct methods such as gel-electrophoresis and DNA sequencing, mutations can also be detected by *in situ* analysis.

5 Altered levels of CRIK also can be detected in various tissues. Assays used to detect levels of the receptor polypeptides in a body sample, such as blood or a tissue biopsy, derived from a host are well known to those of skill in the art and include radioimmunoassays, competitive binding assays, Western blot analysis, and ELISA assays.

10

All patents and patent applications cited in this disclosure are expressly incorporated herein by reference. The above disclosure generally describes the present invention. A more complete understanding can be obtained by reference to the following specific examples, which are provided for purposes of illustration only and are not
15 intended to limit the scope of the invention.

EXAMPLE 1

Detection of human citron rho/rac-interacting kinase activity

20 Subconfluent COS7 cells in 10-cm dishes are transiently transfected by the DEAE-dextran/chloroquine method with 10 µg of FLAG-SEQ ID NO: 1 vector. Cells are harvested 48 h after transfection. Immunoblotting is performed, and cells are probed with anti-FLAG M2 antibodies (Eastman Kodak Co.) Blots are developed using horseradish peroxidase-conjugated secondary antibodies and ECL detection system
25 (Amersham Pharmacia Biotech). In vitro kinase assays are performed by incubating immune complexes in 50 µl of kinase buffer (50 mM HEPES, pH 7.4, 5 mM MgCl₂, 3 mM MnCl₂, 1mM dithiothreitol), in the presence or absence of 5 µg of histone H1 or myelin basic protein, plus 0.1 mM ATP and 10 mCi of [gamma-32P] ATP (6000 Ci/mM, NEN Life Science Products) for 30 min at 30 °C. The products are
30 analyzed by 5% or 12.5% SDS-PAGE followed by autoradiography. For immunoprecipitation of metabolically labeled proteins, primary keratinocytes are

incubated with 0.1 mCi/ml [35S]methionine (Expre35S; NEN Life Science Products) for 4 h in methionine-free medium in the presence of serum. Immunoprecipitated proteins are separated on a 5% SDS-PAGE gel and visualized by autoradiography. It is shown that the polypeptide of SEQ ID NO: 2 has a human citron rho/rac-interacting kinase-short kinase activity.

EXAMPLE 2

Expression of recombinant human CRIK

The *Pichia pastoris* expression vector pPICZB (Invitrogen, San Diego, CA) is used to produce large quantities of recombinant human CRIK polypeptides in yeast. The CRIK-encoding DNA sequence is derived from SEQ ID NO:1. Before insertion into vector pPICZB, the DNA sequence is modified by well known methods in such a way that it contains at its 5'-end an initiation codon and at its 3'-end an enterokinase cleavage site, a His6 reporter tag and a termination codon. Moreover, at both termini recognition sequences for restriction endonucleases are added and after digestion of the multiple cloning site of pPICZ B with the corresponding restriction enzymes the modified DNA sequence is ligated into pPICZB. This expression vector is designed for inducible expression in *Pichia pastoris*, driven by a yeast promoter. The resulting pPICZ/md-His6 vector is used to transform the yeast.

The yeast is cultivated under usual conditions in 5 liter shake flasks and the recombinantly produced protein isolated from the culture by affinity chromatography (Ni-NTA-Resin) in the presence of 8 M urea. The bound polypeptide is eluted with buffer, pH 3.5, and neutralized. Separation of the polypeptide from the His6 reporter tag is accomplished by site-specific proteolysis using enterokinase (Invitrogen, San Diego, CA) according to manufacturer's instructions. Purified human CRIK polypeptide is obtained.

EXAMPLE 3*Identification of test compounds that bind to CRIK polypeptides*

Purified CRIK polypeptides comprising a glutathione-S-transferase protein and
5 absorbed onto glutathione-derivatized wells of 96-well microtiter plates are contacted
with test compounds from a small molecule library at pH 7.0 in a physiological
buffer solution. Human CRIK polypeptides comprise the amino acid sequence
shown in SEQ ID NO:2. The test compounds comprise a fluorescent tag. The
10 samples are incubated for 5 minutes to one hour. Control samples are incubated in
the absence of a test compound.

The buffer solution containing the test compounds is washed from the wells.
Binding of a test compound to a CRIK polypeptide is detected by fluorescence
measurements of the contents of the wells. A test compound that increases the
15 fluorescence in a well by at least 15% relative to fluorescence of a well in which a
test compound is not incubated is identified as a compound which binds to a CRIK
polypeptide.

EXAMPLE 4*Identification of a test compound which decreases CRIK gene expression*

A test compound is administered to a culture of human cells transfected with a CRIK
expression construct and incubated at 37 °C for 10 to 45 minutes. A culture of the
same type of cells that have not been transfected is incubated for the same time
25 without the test compound to provide a negative control.

RNA is isolated from the two cultures as described in Chirgwin *et al.*, *Biochem. 18*,
5294-99, 1979). Northern blots are prepared using 20 to 30 µg total RNA and
hybridized with a ³²P-labeled CRIK-specific probe at 65 °C in Express-hyb
30 (CLONTECH). The probe comprises at least 11 contiguous nucleotides selected
from the complement of SEQ ID NO:1. A test compound that decreases the CRIK-

specific signal relative to the signal obtained in the absence of the test compound is identified as an inhibitor of CRIK gene expression.

EXAMPLE 5

5 *Identification of a test compound which decreases CRIK activity*

A test compound is administered to a culture of human cells transfected with a CRIK expression construct and incubated at 37 °C for 10 to 45 minutes. A culture of the same type of cells that have not been transfected is incubated for the same time
10 without the test compound to provide a negative control. CRIK activity is measured using the method of Di Cunto *et al.*, J Biol Chem. 1998 Nov 6;273(45):29706-11.

A test compound which decreases the CRIK activity of the CRIK relative to the CRIK activity in the absence of the test compound is identified as an inhibitor of
15 CRIK activity.

EXAMPLE 6

Tissue-specific expression of CRIK

20 The qualitative expression pattern of CRIK in various tissues is determined by Reverse Transcription-Polymerase Chain Reaction (RT-PCR).

To demonstrate that CRIK is involved in the disease process of COPD, the initial expression panel consists of RNA samples from respiratory tissues and inflammatory
25 cells relevant to COPD: lung (adult and fetal), trachea, freshly isolated alveolar type II cells, cultured human bronchial epithelial cells, cultured small airway epithelial cells, cultured bronchial smooth muscle cells, cultured H441 cells (Clara-like), freshly isolated neutrophils and monocytes, and cultured monocytes (macrophage-like). Body map profiling also is carried out, using total RNA panels purchased from
30 Clontech. The tissues are adrenal gland, bone marrow, brain, colon, heart, kidney,

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liver, lung, mammary gland, pancreas, prostate, salivary gland, skeletal muscle, small intestine, spleen, stomach, testis, thymus, trachea, thyroid, and uterus.

5 To demonstrate that CRIK is involved in CNS disorders, the following tissues are screened: fetal and adult brain, muscle, heart, lung, kidney, liver, thymus, testis, colon, placenta, trachea, pancreas, kidney, gastric mucosa, colon, liver, cerebellum, skin, cortex (Alzheimer's and normal), hypothalamus, cortex, amygdala, cerebellum, hippocampus, choroid, plexus, thalamus, and spinal cord.

10 To demonstrate that CRIK is involved in the disease process of obesity, expression is determined in the following tissues: subcutaneous adipose tissue, mesenteric adipose tissue, adrenal gland, bone marrow, brain (cerebellum, spinal cord, cerebral cortex, caudate, medulla, substantia nigra, and putamen), colon, fetal brain, heart, kidney, liver, lung, mammary gland, pancreas, placenta, prostate, salivary gland, skeletal
15 muscle small intestine, spleen, stomach, testes, thymus, thyroid trachea, and uterus. Neuroblastoma cell lines SK-Nr-Be (2), Hr, Sk-N-As, HTB-10, IMR-32, SNSY-5Y, T3, SK-N-D2, D283, DAOY, CHP-2, U87MG, BE(2)C, T986, KANTS, MO59K, CHP234, C6 (rat), SK-N-F1, SK-PU-DW, PFSK-1, BE(2)M17, and MCIXC also are tested for CRIK expression. As a final step, the expression of CRIK in cells derived
20 from normal individuals with the expression of cells derived from obese individuals is compared.

Quantitative expression profiling. Quantitative expression profiling is performed by the form of quantitative PCR analysis called "kinetic analysis" firstly described in
25 Higuchi *et al.*, *BioTechnology* 10, 413-17, 1992, and Higuchi *et al.*, *BioTechnology* 11, 1026-30, 1993. The principle is that at any given cycle within the exponential phase of PCR, the amount of product is proportional to the initial number of template copies.

30 If the amplification is performed in the presence of an internally quenched fluorescent oligonucleotide (TaqMan probe) complementary to the target sequence,

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the probe is cleaved by the 5'-3' endonuclease activity of Taq DNA polymerase and a fluorescent dye released in the medium (Holland *et al.*, *Proc. Natl. Acad. Sci. U.S.A.* 88, 7276-80, 1991). Because the fluorescence emission will increase in direct proportion to the amount of the specific amplified product, the exponential growth phase of PCR product can be detected and used to determine the initial template concentration (Heid *et al.*, *Genome Res.* 6, 986-94, 1996, and Gibson *et al.*, *Genome Res.* 6, 995-1001, 1996).

The amplification of an endogenous control can be performed to standardize the amount of sample RNA added to a reaction. In this kind of experiment, the control of choice is the 18S ribosomal RNA. Because reporter dyes with differing emission spectra are available, the target and the endogenous control can be independently quantified in the same tube if probes labeled with different dyes are used.

All "real time PCR" measurements of fluorescence are made in the ABI Prism 7700.

RNA extraction and cDNA preparation. Total RNA from the tissues listed above are used for expression quantification. RNAs labeled "from autopsy" were extracted from autaptic tissues with the TRIzol reagent (Life Technologies, MD) according to the manufacturer's protocol.

Fifty µg of each RNA were treated with DNase I for 1 hour at 37°C in the following reaction mix: 0.2 U/µl RNase-free DNase I (Roche Diagnostics, Germany); 0.4 U/µl RNase inhibitor (PE Applied Biosystems, CA); 10 mM Tris-HCl pH 7.9; 10mM MgCl₂; 50 mM NaCl; and 1 mM DTT.

After incubation, RNA is extracted once with 1 volume of phenol:chloroform:isoamyl alcohol (24:24:1) and once with chloroform, and precipitated with 1/10 volume of 3 M NaAcetate, pH5.2, and 2 volumes of ethanol.

Fifty μ g of each RNA from the autaptic tissues are DNase treated with the DNA-free kit purchased from Ambion (Ambion, TX). After resuspension and spectrophotometric quantification, each sample is reverse transcribed with the TaqMan Reverse Transcription Reagents (PE Applied Biosystems, CA) according to the manufacturer's protocol. The final concentration of RNA in the reaction mix is 200ng/ μ L. Reverse transcription is carried out with 2.5 μ M of random hexamer primers.

TaqMan quantitative analysis. Specific primers and probe are designed according to the recommendations of PE Applied Biosystems; the probe can be labeled at the 5' end FAM (6-carboxy-fluorescein) and at the 3' end with TAMRA (6-carboxy-tetramethyl-rhodamine). Quantification experiments are performed on 10 ng of reverse transcribed RNA from each sample. Each determination is done in triplicate.

Total cDNA content is normalized with the simultaneous quantification (multiplex PCR) of the 18S ribosomal RNA using the Pre-Developed TaqMan Assay Reagents (PDAR) Control Kit (PE Applied Biosystems, CA).

The assay reaction mix is as follows: 1X final TaqMan Universal PCR Master Mix (from 2X stock) (PE Applied Biosystems, CA); 1X PDAR control – 18S RNA (from 20X stock); 300 nM forward primer; 900 nM reverse primer; 200 nM probe; 10 ng cDNA; and water to 25 μ L.

Each of the following steps are carried out once: pre PCR, 2 minutes at 50 °C, and 10 minutes at 95 °C. The following steps are carried out 40 times: denaturation, 15 seconds at 95 °C, annealing/extension, 1 minute at 60 °C.

The experiment is performed on an ABI Prism 7700 Sequence Detector (PE Applied Biosystems, CA). At the end of the run, fluorescence data acquired during PCR are processed as described in the ABI Prism 7700 user's manual in order to achieve better background subtraction as well as signal linearity with the starting target quantity.

EXAMPLE 7*Identification of test compound efficacy in a COPD animal model*

5 Guinea pigs are exposed on a single occasion to tobacco smoke for 50 minutes. Animals are sacrificed between 10 minutes and 24 hour following the end of the exposure and their lungs placed in RNAlater™. The lung tissue is homogenized, and total RNA was extracted using a Qiagen RNeasy™ Maxi kit. Molecular Probes RiboGreen™ RNA quantitation method is used to quantify the amount of RNA in
10 each sample.

Total RNA is reverse transcribed, and the resultant cDNA is used in a real-time polymerase chain reaction (PCR). The cDNA is added to a solution containing the sense and anti-sense primers and the 6-carboxy-tetramethyl-rhodamine labelled probe
15 of the CRIK gene. Cyclophilin is used as the housekeeping gene. The expression of the CRIK gene is measured using the TaqMan real-time PCR system that generates an amplification curve for each sample. From this curve a threshold cycle value is calculated: the fractional cycle number at which the amount of amplified target reaches a fixed threshold. A sample containing many copies of the CRIK gene will
20 reach this threshold earlier than a sample containing fewer copies. The threshold is set at 0.2, and the threshold cycle C_T is calculated from the amplification curve. The C_T value for the CRIK gene is normalized using the C_T value for the housekeeping gene.

25 Expression of the CRIK gene is increased by at least 3-fold between 10 minutes and 3 hours post tobacco smoke exposure compared to air exposed control animals.

Test compounds are evaluated as follows. Animals are pre-treated with a test compound between 5 minutes and 1 hour prior to the tobacco smoke exposure and
30 they are then sacrificed up to 3 hours after the tobacco smoke exposure has been completed. Control animals are pre-treated with the vehicle of the test compound via

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the route of administration chosen for the test compound. A test compound that reduces the tobacco smoke induced upregulation of CRIK gene relative to the expression seen in vehicle treated tobacco smoke exposed animals is identified as an inhibitor of CRIK gene expression.

5

EXAMPLE 8***Expression of human citron rho/rac-interacting kinase***

10 Total RNA used for Taqman quantitative analysis were either purchased (Clontech,CA) or extracted from tissues using TRIzol reagent (Life Technologies, MD) according to a modified vendor protocol which utilizes the Rneasy protocol (Qiagen, CA). One hundred µg of each RNA were treated with DNase I using RNase free- DNase (Qiagen, CA) for use with RNeasy or QiaAmp columns.

15 After elution and quantitation with Ribogreen (Molecular Probes Inc., OR), each sample was reverse transcribed using the GibcoBRL Superscript II First Strand Synthesis System for RT-PCR according to vendor protocol (Life Technologies, MD). The final concentration of RNA in the reaction mix was 50ng/µL. Reverse transcription was performed with 50 ng of random hexamers.

20

Specific primers and probe were designed according to PE Applied Biosystems' Primer Express program recommendations and are listed below:

forward primer: 5'-(TCCAATTTTGATGAACCAGAGAAG)-3'

25

reverse primer: 5'-(AACCCCACAAACGGCAGTT)-3'

probe: SYBR Green

Quantitation experiments were performed on 25 ng of reverse transcribed RNA from each sample. 18S ribosomal RNA was measured as a control using the Pre-
30 Developed TaqMan Assay Reagents (PDAR)(PE Applied Biosystems, CA). The assay reaction mix was as follows:

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		final
	TaqMan SYBR Green PCR Master Mix (2x)	1x
	(PE Applied Biosystems, CA)	
5	Forward primer	300nM
	Reverse primer	300nM
	cDNA	25ng
	Water to 25uL	
	PCR conditions:	
10	Once: 2' minutes at 50° C	
	10 minutes at 95°C	
	40cycles: 15 sec.at 95°C	
	1 minute at 60°C	
15	The experiment was performed on an ABI Prism 7700 Sequence Detector (PE Applied Biosystems, CA). At the end of the run, fluorescence data acquired during PCR were processed as described in the ABI Prism 7700 user's manual. Fold change was calculated using the delta-delta CT method with normalization to the 18S values. Relative expression was calculated by normalizing to 18s (D Ct), then making the	
20	highest expressing tissue 100 and everything else relative to it. Copy number conversion was performed without normalization using the formula $C_n = 10^{(C_t - 40.007)/-3.623}$.	
	The results are shown in FIG. 21.	
25	Human citron rho/rac-interacting kinase expressed in adipose and skeletal muscle could be regulated to increase insulin sensitivity.	

EXAMPLE 9*In vivo testing of compounds/target validation***1. Pain:*****Acute Pain***

5

Acute pain is measured on a hot plate mainly in rats. Two variants of hot plate testing are used: In the classical variant animals are put on a hot surface (52 to 56 °C) and the latency time is measured until the animals show nocifensive behavior, such as stepping or foot licking. The other variant is an increasing temperature hot plate where the experimental animals are put on a surface of neutral temperature. Subsequently this surface is slowly but constantly heated until the animals begin to lick a hind paw. The temperature which is reached when hind paw licking begins is a measure for pain threshold.

10

15

Compounds are tested against a vehicle treated control group. Substance application is performed at different time points via different application routes (i.v., i.p., p.o., i.t., i.c.v., s.c., intradermal, transdermal) prior to pain testing.

Persistent Pain

20

Persistent pain is measured with the formalin or capsaicin test, mainly in rats. A solution of 1 to 5% formalin or 10 to 100 µg capsaicin is injected into one hind paw of the experimental animal. After formalin or capsaicin application the animals show nocifensive reactions like flinching, licking and biting of the affected paw. The number of nocifensive reactions within a time frame of up to 90 minutes is a measure for intensity of pain.

25

Compounds are tested against a vehicle treated control group. Substance application is performed at different time points via different application routes (i.v., i.p., p.o., i.t., i.c.v., s.c., intradermal, transdermal) prior to formalin or capsaicin administration.

30

Neuropathic Pain

Neuropathic pain is induced by different variants of unilateral sciatic nerve injury mainly in rats. The operation is performed under anesthesia. The first variant of sciatic nerve injury is produced by placing loosely constrictive ligatures around the common sciatic nerve. The second variant is the tight ligation of about the half of the diameter of the common sciatic nerve. In the next variant, a group of models is used in which tight ligations or transections are made of either the L5 and L6 spinal nerves, or the L₄ spinal nerve only. The fourth variant involves an axotomy of two of the three terminal branches of the sciatic nerve (tibial and common peroneal nerves) leaving the remaining sural nerve intact whereas the last variant comprises the axotomy of only the tibial branch leaving the sural and common nerves uninjured. Control animals are treated with a sham operation.

Postoperatively, the nerve injured animals develop a chronic mechanical allodynia, cold allodynia, as well as a thermal hyperalgesia. Mechanical allodynia is measured by means of a pressure transducer (electronic von Frey Anesthesiometer, IITC Inc.-Life Science Instruments, Woodland Hills, SA, USA; Electronic von Frey System, Somedic Sales AB, Hörby, Sweden). Thermal hyperalgesia is measured by means of a radiant heat source (Plantar Test, Ugo Basile, Comerio, Italy), or by means of a cold plate of 5 to 10 °C where the nocifensive reactions of the affected hind paw are counted as a measure of pain intensity. A further test for cold induced pain is the counting of nocifensive reactions, or duration of nocifensive responses after plantar administration of acetone to the affected hind limb. Chronic pain in general is assessed by registering the circadian rhythms in activity (Surjo and Arndt, Universität zu Köln, Cologne, Germany), and by scoring differences in gait (foot print patterns; FOOTPRINTS program, Klapdor et al., 1997. A low cost method to analyze footprint patterns. J. Neurosci. Methods 75, 49-54).

Compounds are tested against sham operated and vehicle treated control groups. Substance application is performed at different time points via different application routes (i.v., i.p., p.o., i.t., i.c.v., s.c., intradermal, transdermal) prior to pain testing.

5 *Inflammatory Pain*

Inflammatory pain is induced mainly in rats by injection of 0.75 mg carrageenan or complete Freund's adjuvant into one hind paw. The animals develop an edema with mechanical allodynia as well as thermal hyperalgesia. Mechanical allodynia is measured by means of a pressure transducer (electronic von Frey Anesthesiometer, IITC Inc.-Life Science Instruments, Woodland Hills, SA, USA). Thermal hyperalgesia is measured by means of a radiant heat source (Plantar Test, Ugo Basile, Comerio, Italy, Paw thermal stimulator, G. Ozaki, University of California, USA). For edema measurement two methods are being used. In the first method, the animals are sacrificed and the affected hindpaws sectioned and weighed. The second method comprises differences in paw volume by measuring water displacement in a plethysmometer (Ugo Basile, Comerio, Italy).

Compounds are tested against uninflamed as well as vehicle treated control groups. Substance application is performed at different time points via different application routes (i.v., i.p., p.o., i.t., i.c.v., s.c., intradermal, transdermal) prior to pain testing.

Diabetic Neuropathic Pain

Rats treated with a single intraperitoneal injection of 50 to 80 mg/kg streptozotocin develop a profound hyperglycemia and mechanical allodynia within 1 to 3 weeks. Mechanical allodynia is measured by means of a pressure transducer (electronic von Frey Anesthesiometer, IITC Inc.-Life Science Instruments, Woodland Hills, SA, USA).

Compounds are tested against diabetic and non-diabetic vehicle treated control groups. Substance application is performed at different time points via different application routes (i.v., i.p., p.o., i.t., i.c.v., s.c., intradermal, transdermal) prior to pain testing.

5

2. Parkinson's disease

6-Hydroxydopamine (6-OH-DA) Lesion

10

Degeneration of the dopaminergic nigrostriatal and striatopallidal pathways is the central pathological event in Parkinson's disease. This disorder has been mimicked experimentally in rats using single/sequential unilateral stereotaxic injections of 6-OH-DA into the medium forebrain bundle (MFB).

15

Male Wistar rats (Harlan Winkelmann, Germany), weighing 200 ± 250 g at the beginning of the experiment, are used. The rats are maintained in a temperature- and humidity-controlled environment under a 12 h light/dark cycle with free access to food and water when not in experimental sessions. The following in vivo protocols are approved by the governmental authorities. All efforts are made to minimize animal suffering, to reduce the number of animals used, and to utilize alternatives to in vivo techniques.

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25

Animals are administered pargyline on the day of surgery (Sigma, St. Louis, MO, USA; 50 mg/kg i.p.) in order to inhibit metabolism of 6-OHDA by monoamine oxidase and desmethylinipramine HCl (Sigma; 25 mg/kg i.p.) in order to prevent uptake of 6-OHDA by noradrenergic terminals. Thirty minutes later the rats are anesthetized with sodium pentobarbital (50 mg/kg) and placed in a stereotaxic frame. In order to lesion the DA nigrostriatal pathway 4 μ l of 0.01% ascorbic acid-saline containing 8 μ g of 6-OHDA HBr (Sigma) are injected into the left medial fore-brain bundle at a rate of 1 μ l/min (2.4 mm anterior, 1.49 mm lateral, -2.7 mm ventral to Bregma and the skull surface). The needle is left in place an additional 5 min to allow diffusion to occur.

30

Stepping Test

Forelimb akinesia is assessed three weeks following lesion placement using a modified stepping test protocol. In brief, the animals are held by the experimenter with one hand fixing the hindlimbs and slightly raising the hind part above the surface. One paw is touching the table, and is then moved slowly sideways (5 s for 1 m), first in the forehand and then in the backhand direction. The number of adjusting steps is counted for both paws in the backhand and forehand direction of movement. The sequence of testing is right paw forehand and backhand adjusting stepping, followed by left paw forehand and backhand directions. The test is repeated three times on three consecutive days, after an initial training period of three days prior to the first testing. Forehand adjusted stepping reveals no consistent differences between lesioned and healthy control animals. Analysis is therefore restricted to backhand adjusted stepping.

Balance Test

Balance adjustments following postural challenge are also measured during the stepping test sessions. The rats are held in the same position as described in the stepping test and, instead of being moved sideways, tilted by the experimenter towards the side of the paw touching the table. This maneuver results in loss of balance and the ability of the rats to regain balance by forelimb movements is scored on a scale ranging from 0 to 3. Score 0 is given for a normal forelimb placement. When the forelimb movement is delayed but recovery of postural balance detected, score 1 is given. Score 2 represents a clear, yet insufficient, forelimb reaction, as evidenced by muscle contraction, but lack of success in recovering balance, and score 3 is given for no reaction of movement. The test is repeated three times a day on each side for three consecutive days after an initial training period of three days prior to the first testing.

Staircase Test (Paw Reaching)

A modified version of the staircase test is used for evaluation of paw reaching behavior three weeks following primary and secondary lesion placement. Plexiglass test boxes with a central platform and a removable staircase on each side are used. The apparatus is designed such that only the paw on the same side at each staircase can be used, thus providing a measure of independent forelimb use. For each test the animals are left in the test boxes for 15 min. The double staircase is filled with 7 x 3 chow pellets (Precision food pellets, formula: P, purified rodent diet, size 45 mg; Sandown Scientific) on each side. After each test the number of pellets eaten (successfully retrieved pellets) and the number of pellets taken (touched but dropped) for each paw and the success rate (pellets eaten/pellets taken) are counted separately. After three days of food deprivation (12 g per animal per day) the animals are tested for 11 days. Full analysis is conducted only for the last five days.

MPTP treatment

The neurotoxin 1-methyl-4-phenyl-1,2,3,6-tetrahydro-pyridine (MPTP) causes degeneration of mesencephalic dopaminergic (DAergic) neurons in rodents, non-human primates, and humans and, in so doing, reproduces many of the symptoms of Parkinson's disease. MPTP leads to a marked decrease in the levels of dopamine and its metabolites, and in the number of dopaminergic terminals in the striatum as well as severe loss of the tyrosine hydroxylase (TH)-immunoreactive cell bodies in the substantia nigra, pars compacta.

In order to obtain severe and long-lasting lesions, and to reduce mortality, animals receive single injections of MPTP, and are then tested for severity of lesion 7–10 days later. Successive MPTP injections are administered on days 1, 2 and 3. Animals receive application of 4 mg/kg MPTP hydrochloride (Sigma) in saline once daily. All injections are intraperitoneal (i.p.) and the MPTP stock solution is frozen between injections. Animals are decapitated on day 11.

Immunohistology

At the completion of behavioral experiments, all animals are anaesthetized with 3 ml
5 thiopental (1 g/40 ml i.p., Tyrol Pharma). The mice are perfused transcardially with
0.01 M PBS (pH 7.4) for 2 min, followed by 4% paraformaldehyde (Merck) in PBS
for 15 min. The brains are removed and placed in 4% paraformaldehyde for 24 h at
4 °C. For dehydration they are then transferred to a 20% sucrose (Merck) solution in
0.1 M PBS at 4 °C until they sink. The brains are frozen in methylbutan at -20 °C for
10 2 min and stored at -70 °C. Using a sledge microtome (mod. 3800-Frigocut, Leica),
25 µm sections are taken from the genu of the corpus callosum (AP 1.7 mm) to the
hippocampus (AP 21.8 mm) and from AP 24.16 to AP 26.72. Forty-six sections are
cut and stored in assorters in 0.25 M Tris buffer (pH 7.4) for immunohistochemistry.

15 A series of sections is processed for free-floating tyrosine hydroxylase (TH)
immunohistochemistry. Following three rinses in 0.1 M PBS, endogenous per-
oxidase activity is quenched for 10 min in 0.3% H₂O₂ ±PBS. After rinsing in PBS,
sections are preincubated in 10% normal bovine serum (Sigma) for 5 min as blocking
agent and transferred to either primary anti-rat TH rabbit antiserum (dilution 1:2000).

20 Following overnight incubation at room temperature, sections for TH immuno-
reactivity are rinsed in PBS (2 x10 min) and incubated in biotinylated anti-rabbit
immunoglobulin G raised in goat (dilution 1:200) (Vector) for 90 min, rinsed
repeatedly and transferred to Vectastain ABC (Vector) solution for 1 h. 3,3'
25 -Diaminobenzidine tetrahydrochloride (DAB; Sigma) in 0.1 M PBS, supplemented
with 0.005% H₂O₂ , serves as chromogen in the subsequent visualization reaction.
Sections are mounted on to gelatin-coated slides, left to dry overnight,
counter-stained with hematoxylin dehydrated in ascending alcohol concentrations
and cleared in butylacetate. Coverslips are mounted on entellan.

Rotarod Test

We use a modification of the procedure described by Rozas and Labandeira-Garcia (1997), with a CR-1 Rotamex system (Columbus Instruments, Columbus, OH) comprising an IBM-compatible personal computer, a CIO-24 data acquisition card, a control unit, and a four-lane rotarod unit. The rotarod unit consists of a rotating spindle (diameter 7.3 cm) and individual compartments for each mouse. The system software allows preprogramming of session protocols with varying rotational speeds (0–80 rpm). Infrared beams are used to detect when a mouse has fallen onto the base grid beneath the rotarod. The system logs the fall as the end of the experiment for that mouse, and the total time on the rotarod, as well as the time of the fall and all the set-up parameters, are recorded. The system also allows a weak current to be passed through the base grid, to aid training.

3. Dementia

The object recognition task

The object recognition task has been designed to assess the effects of experimental manipulations on the cognitive performance of rodents. A rat is placed in an open field, in which two identical objects are present. The rats inspects both objects during the first trial of the object recognition task. In a second trial, after a retention interval of for example 24 hours, one of the two objects used in the first trial, the ‘familiar’ object, and a novel object are placed in the open field. The inspection time at each of the objects is registered. The basic measures in the OR task is the time spent by a rat exploring the two object the second trial. Good retention is reflected by higher exploration times towards the novel than the ‘familiar’ object.

Administration of the putative cognition enhancer prior to the first trial predominantly allows assessment of the effects on acquisition, and eventually on consolidation processes. Administration of the testing compound after the first trial

allows to assess the effects on consolidation processes, whereas administration before the second trial allows to measure effects on retrieval processes.

The passive avoidance task

5

The passive avoidance task assesses memory performance in rats and mice. The inhibitory avoidance apparatus consists of a two-compartment box with a light compartment and a dark compartment. The two compartments are separated by a guillotine door that can be operated by the experimenter. A threshold of 2 cm
10 separates the two compartments when the guillotine door is raised. When the door is open, the illumination in the dark compartment is about 2 lux. The light intensity is about 500 lux at the center of the floor of the light compartment.

Two habituation sessions, one shock session, and a retention session are given,
15 separated by inter-session intervals of 24 hours. In the habituation sessions and the retention session the rat is allowed to explore the apparatus for 300 sec. The rat is placed in the light compartment, facing the wall opposite to the guillotine door. After an accommodation period of 15 sec. the guillotine door is opened so that all parts of the apparatus can be visited freely. Rats normally avoid brightly lit areas and will
20 enter the dark compartment within a few seconds.

In the shock session the guillotine door between the compartments is lowered as soon as the rat has entered the dark compartment with its four paws, and a scrambled 1 mA footshock is administered for 2 sec. The rat is removed from the apparatus and
25 put back into its home cage. The procedure during the retention session is identical to that of the habituation sessions.

The step-through latency, that is the first latency of entering the dark compartment (in sec.) during the retention session is an index of the memory performance of the
30 animal; the longer the latency to enter the dark compartment, the better the retention is. A testing compound is given half an hour before the shock session, together with

1 mg*kg⁻¹ scopolamine. Scopolamine impairs the memory performance during the retention session 24 hours later. If the test compound increases the enter latency compared with the scopolamine-treated controls, is likely to possess cognition enhancing potential.

5

The Morris water escape task

The Morris water escape task measures spatial orientation learning in rodents. It is a test system that has extensively been used to investigate the effects of putative
10 therapeutic on the cognitive functions of rats and mice. The performance of an animal is assessed in a circular water tank with an escape platform that is submerged about 1 cm below the surface of the water. The escape platform is not visible for an animal swimming in the water tank. Abundant extra-maze cues are provided by the furniture in the room, including desks, computer equipment, a second water tank, the
15 presence of the experimenter, and by a radio on a shelf that is playing softly.

The animals receive four trials during five daily acquisition sessions. A trial is started by placing an animal into the pool, facing the wall of the tank. Each of four starting positions in the quadrants north, east, south, and west is used once in a series of four
20 trials; their order is randomized. The escape platform is always in the same position. A trial is terminated as soon as the animal had climbs onto the escape platform or when 90 seconds have elapsed, whichever event occurs first. The animal is allowed to stay on the platform for 30 seconds. Then it is taken from the platform and the next trial is started. If an animal did not find the platform within 90 seconds it is put
25 on the platform by the experimenter and is allowed to stay there for 30 seconds. After the fourth trial of the fifth daily session, an additional trial is given as a probe trial: the platform is removed, and the time the animal spends in the four quadrants is measured for 30 or 60 seconds. In the probe trial, all animals start from the same start
30 position, opposite to the quadrant where the escape platform had been positioned during acquisition.

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- Four different measures are taken to evaluate the performance of an animal during acquisition training: escape latency, traveled distance, distance to platform, and swimming speed. The following measures are evaluated for the probe trial: time (s) in quadrants and traveled distance (cm) in the four quadrants. The probe trial provides additional information about how well an animal learned the position of the escape platform. If an animal spends more time and swims a longer distance in the quadrant where the platform had been positioned during the acquisition sessions than in any other quadrant, one concludes that the platform position has been learned well.
- 10 In order to assess the effects of putative cognition enhancing compounds, rats or mice with specific brain lesions which impair cognitive functions, or animals treated with compounds such as scopolamine or MK-801, which interfere with normal learning, or aged animals which suffer from cognitive deficits, are used.

The T-maze spontaneous alternation task

The T-maze spontaneous alternation task (TeMCAT) assesses the spatial memory performance in mice. The start arm and the two goal arms of the T-maze are provided with guillotine doors which can be operated manually by the experimenter. A mouse is put into the start arm at the beginning of training. The guillotine door is closed. In the first trial, the 'forced trial', either the left or right goal arm is blocked by lowering the guillotine door. After the mouse has been released from the start arm, it will negotiate the maze, eventually enter the open goal arm, and return to the start position, where it will be confined for 5 seconds, by lowering the guillotine door. Then, the animal can choose freely between the left and right goal arm (all guillotine-doors opened) during 14 'free choice' trials. As soon as the mouse has entered one goal arm, the other one is closed. The mouse eventually returns to the start arm and is free to visit whichever goal arm it wants after having been confined to the start arm for 5 seconds. After completion of 14 free choice trials in one session, the animal is removed from the maze. During training, the animal is never handled.

The percent alternations out of 14 trials is calculated. This percentage and the total time needed to complete the first forced trial and the subsequent 14 free choice trials (in s) is analyzed. Cognitive deficits are usually induced by an injection of scopolamine, 30 min before the start of the training session. Scopolamine reduced the per-cent alternations to chance level, or below. A cognition enhancer, which is always administered before the training session, will at least partially, antagonize the scopolamine-induced reduction in the spontaneous alternation rate.

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CLAIMS

1. An isolated polynucleotide being selected from the group consisting of:
 - a. a polynucleotide encoding a human citron rho/rac-interacting kinase polypeptide comprising an amino acid sequence selected from the group consisting of:
 - i. amino acid sequences which are at least about 97% identical to the amino acid sequence shown in SEQ ID NO: 2; and
 - ii. the amino acid sequence shown in SEQ ID NO: 2.
 - b. a polynucleotide comprising the sequence of SEQ ID NOS: 1 or 24;
 - c. a polynucleotide which hybridizes under stringent conditions to a polynucleotide specified in (a) and (b) and encodes a human citron rho/rac-interacting kinase polypeptide;
 - d. a polynucleotide the sequence of which deviates from the polynucleotide sequences specified in (a) to (c) due to the degeneration of the genetic code and encodes a human citron rho/rac-interacting kinase polypeptide; and
 - e. a polynucleotide which represents a fragment, derivative or allelic variation of a polynucleotide sequence specified in (a) to (d) and encodes a human citron rho/rac-interacting kinase polypeptide.
2. An expression vector containing any polynucleotide of claim 1.
3. A host cell containing the expression vector of claim 2.
4. A substantially purified human citron rho/rac-interacting kinase polypeptide encoded by a polynucleotide of claim 1.
5. A method for producing a human citron rho/rac-interacting kinase polypeptide, wherein the method comprises the following steps:

- a. culturing the host cell of claim 3 under conditions suitable for the expression of the human citron rho/rac-interacting kinase polypeptide; and
 - b. recovering the human citron rho/rac-interacting kinase polypeptide from the host cell culture.
- 5
6. A method for detection of a polynucleotide encoding a human citron rho/rac-interacting kinase polypeptide in a biological sample comprising the following steps:
 - 10 a. hybridizing any polynucleotide of claim 1 to a nucleic acid material of a biological sample, thereby forming a hybridization complex; and
 - b. detecting said hybridization complex.
7. The method of claim 6, wherein before hybridization, the nucleic acid material of the biological sample is amplified.
- 15
8. A method for the detection of a polynucleotide of claim 1 or a human citron rho/rac-interacting kinase polypeptide of claim 4 comprising the steps of:
 - 20 a. contacting a biological sample with a reagent which specifically interacts with the polynucleotide or the human citron rho/rac-interacting kinase polypeptide and
 - b. detecting the interaction
9. A diagnostic kit for conducting the method of any one of claims 6 to 8.
- 25
10. A method of screening for agents which decrease the activity of a human citron rho/rac-interacting kinase, comprising the steps of:
 - 30 a. contacting a test compound with any human citron rho/rac-interacting kinase polypeptide encoded by any polynucleotide of claim 1;
 - b. detecting binding of the test compound to the human citron rho/rac-interacting kinase polypeptide, wherein a test compound which binds

to the polypeptide is identified as a potential therapeutic agent for decreasing the activity of a human citron rho/rac-interacting kinase.

11. A method of screening for agents which regulate the activity of a human citron rho/rac-interacting kinase, comprising the steps of:
- a. contacting a test compound with a human citron rho/rac-interacting kinase polypeptide encoded by any polynucleotide of claim 1; and
 - b. detecting a human citron rho/rac-interacting kinase activity of the polypeptide, wherein a test compound which increases the human citron rho/rac-interacting kinase activity is identified as a potential therapeutic agent for increasing the activity of the human citron rho/rac-interacting kinase, and wherein a test compound which decreases the human citron rho/rac-interacting kinase activity of the polypeptide is identified as a potential therapeutic agent for decreasing the activity of the human citron rho/rac-interacting kinase.
12. A method of screening for agents which decrease the activity of a human citron rho/rac-interacting kinase, comprising the steps of:
- a. contacting a test compound with any polynucleotide of claim 1 and detecting binding of the test compound to the polynucleotide, wherein a test compound which binds to the polynucleotide is identified as a potential therapeutic agent for decreasing the activity of human citron rho/rac-interacting kinase.
13. A method of reducing the activity of human citron rho/rac-interacting kinase, comprising the steps of:
- a. contacting a cell with a reagent which specifically binds to any polynucleotide of claim 1 or any human citron rho/rac-interacting kinase polypeptide of claim 4, whereby the activity of human citron rho/rac-interacting kinase is reduced.

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14. A reagent that modulates the activity of a human citron rho/rac-interacting kinase polypeptide or a polynucleotide wherein said reagent is identified by the method of any of the claim 10 to 12.
- 5 15. A pharmaceutical composition, comprising:
 - a. the expression vector of claim 2 or the reagent of claim 14 and a pharmaceutically acceptable carrier.
- 10 16. *Use of the expression vector of claim 2 or the reagent of claim 14 in the preparation of a medicament for modulating the activity of a human citron rho/rac-interacting kinase in a disease.*
17. Use of claim 16 wherein the disease is obesity, a CNS disorder or COPD.

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Fig. 1

atgttgaagt	tcaaatatgg	agcgcggaat	cctttggatg	ctggtgctgc	tgaacccatt	60
gccagccggg	cctccaggct	gaatctgttc	ttccagggga	aaccaccctt	tatgactcaa	120
cagcagatgt	ctcctctttc	ccgagaaggg	atattagatg	ccctctttgt	tctctttgaa	180
gaatgcagtc	agcctgctct	gatgaagatt	aagcacgtga	gcaactttgt	ccggaagtat	240
tccgacacca	tagctgagtt	acaggagctc	cagccttcgg	caaaggactt	cgaagtcaga	300
agtctttag	gttggtgca	ctttgctgaa	gtgcaggtgg	taagagagaa	agcaaccggg	360
gacatctatg	ctatgaaagt	gatgaagaag	aaggctttat	tggcccagga	gcaggtttca	420
ttttttgagg	aagagcggaa	catattatct	cgaagcacia	gcccgtagg	cccccaatta	480
cagtatgcct	ttcaggacaa	aaatcacctt	tatctgggtc	tgggaatatc	gcctggagg	540
gacttgctgt	cacttttgaa	tagatatgag	gaccagttag	atgaaaacct	gatacagttt	600
tacctagctg	agctgatttt	ggctgttcac	agcgttcac	tgatgggata	cgtgcacga	660
gacatcaagc	ctgagaacat	tctcgttgac	cgcacaggac	acatcaagct	ggtaggattt	720
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ttgttgtgcg	gccagaaaga	gagactgaag	tttgaaggtc	tttgctgcca	tcctttcttc	1080
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tctgacgatg	acacctccaa	ttttgatgaa	ccagagaaga	attcgtgggt	ttcatcctct	1200
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cctgccaaaga	ctagctccat	ggaaaagaaa	cttctcatca	aaagcaaaga	gctacaagac	1380
tctcaggaca	agtgtcacia	gatggagcag	gaaatgaccc	ggttacatcg	gagagtgtca	1440
gaggtggagg	ctgtgcttag	tcagaaggag	gtggagctga	aggcctctga	gactcagaga	1500
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gatatcagag	agcagagccg	gaagctccaa	gaaatcaaag	agcaggagta	ccaggctcaa	1680
gtggaagaaa	tgaggttgat	gatgaatcag	ttggaagagg	atcttgtctc	agcaagaaga	1740
cggagtgatc	tctacgaatc	tgagctgaga	gagtctcggc	ttgctgctga	agaattcaag	1800
cggaaagcga	cagaatgtca	gcataaactg	ttgaaggcta	aggatcaagg	gaagcctgaa	1860
gtgggagaat	atgcgaaact	ggagaagatc	aatgctgagc	agcagctcaa	aattcaggag	1920
ctccaagaga	aactggagaa	ggctgtaaaa	gccagcacgg	aggccaccga	gctgctgcag	1980
aatatccgcc	aggcaaagga	gcgagccgag	agggagctgg	agaagctgca	gaaccgagag	2040
gattcttctg	aaggcatcag	aaagaagctg	gtggaagctg	aggaacgccg	ccattctctg	2100
gagaacaagg	taaagagact	agagaccatg	gagcgtagag	aaaacagact	gaaggatgac	2160
atccagacaa	aatcccaaca	gatccagcag	atggctgata	aaattctgga	gctcgaagag	2220
aaacatcggg	aggcccaagt	ctcagcccag	cacctagaag	tgcacctgaa	acagaaagag	2280

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Fig. 1 (continued)

cagcactatg	aggaaaagat	taaagtgttg	gacaatcaga	taaagaaaga	cctggctgac	2340
aaggagacac	tggagaacat	gatgcagaga	cacgaggagg	aggcccatga	gaagggcaaa	2400
attctcagcg	aacagaaggc	gatgatcaat	gctatggatt	ccaagatcag	atccctggaa	2460
cagaggattg	tggaaactgtc	tgaagccaat	aaacttgtag	caaatagcag	tctttttacc	2520
caaaggaaca	tgaaggccca	agaagagatg	atttctgaac	tcaggcaaca	gaaattttac	2580
ctggagacac	aggctgggaa	gttgagggcc	cagaaccgaa	aactggagga	gcagctggag	2640
aagatcagcc	accaagacca	cagtgcacaag	aatcggctgc	tggaaactgga	gacaagattg	2700
cgggaggtca	gtctagagca	cgaggagcag	aaactggagc	tcaagcgcca	gctcacagag	2760
ctacagctct	ccctgcagga	gcgcgagtca	cagttgacag	ccctgcaggc	tgacgggcg	2820
gccctggaga	gccagcttcg	ccaggcgaag	acagagctgg	aagagaccac	agcagaagct	2880
gaagaggaga	tccaggcact	cacggcacat	agagatgaaa	tccagcgcaa	atttgatgct	2940
cttcgtaaca	gctgtactgt	aatcacagac	ctggaggagc	agctaaacca	gctgaccgag	3000
gacaacgctg	aactcaacaa	ccaaaacttc	tacttgtcca	aacaactcga	tgaggcttct	3060
ggcgccaacg	acgagattgt	acaactgcga	agtgaagtgg	accatctccg	ccgggagatc	3120
acggaacgag	agatgcagct	taccagccag	aagcaaacga	tggaggctct	gaagaccacg	3180
tgcaccatgc	tggaggaaca	ggcatcggat	ttggaggccc	taaacgatga	gctgctagaa	3240
aaagagcggc	agtgggaggc	ctggaggagc	gtcctgggtg	atgagaaatc	ccagtttgag	3300
tgtcgggttc	gagagctgca	gagaatgctg	gacaccgaga	aacagagcag	ggcgagagcc	3360
gatcagcgga	tcaccgagtc	tcgccagggtg	gtggagctgg	cagtgaagga	gcacaaggct	3420
gagattctcg	ctctgcagca	ggctctcaaa	gagcagaagc	tgaaggccga	gagcctctct	3480
gacaagctca	atgacctgga	gaagaagcat	gctatgcttg	aaatgaatgc	ccgaagctta	3540
cagcagaagc	tggagactga	acgagagctc	aaacagaggc	ttctggaaga	gcaagccaaa	3600
ttacagcagc	agatggacct	gcagaaaaat	cacattttcc	gtctgactca	aggactgcaa	3660
gaagctctag	atcgggctga	tctactgaag	acagaaagaa	gtgacttgga	gtatcagctg	3720
gaaaacattc	aggttctcta	ttctcatgaa	aagggtgaaa	tggaaaggcac	tattttctcaa	3780
caaaccaaaac	tcattgattt	tctgcaagcc	aaaatggacc	aacctgctaa	aaagaaaaag	3840
gttcctctgc	agtacaatga	gctgaagctg	gccctggaga	aggagaaagc	tcgctgtgca	3900
gagctagagg	aagcccttca	gaagacccgc	atcgagctcc	ggtccgcccg	ggaggaagct	3960
gcccaccgca	aagcaacgga	ccaccacac	ccatccacgc	cagccaccgc	gaggcagcag	4020
atcgccatgt	ccgccatcgt	gcggtcgcca	gagcaccagc	ccagtgccat	gagcctgctg	4080
gccccgccat	ccagccgcag	aaaggagtct	tcaactccag	aggaatttag	tcggcgtctt	4140
aaggaacgca	tgaccacaa	tattcctcac	cgattcaacg	taggactgaa	catgcgagcc	4200
acaaagtgtg	ctgtgtgtct	ggataccgtg	cactttggac	gccaggcatc	caaattgtctc	4260
gaatgtcagg	tgatgtgtca	ccccaaagtgc	tccacgtgct	tgccagccac	ctgcggcttg	4320
cctgctgaat	atgccacaca	cttcaccgag	gccttctgcc	gtgacaaaat	gaactcccca	4380
ggtctccaga	ccaaggagcc	cagcagcagc	ttgcacctgg	aagggtggat	gaagggtgcc	4440
aggaataaca	aacgaggaca	gcaaggctgg	gacaggaagt	acattgtcct	ggagggatca	4500
aaagtctctca	tttatgacaa	tgaagccaga	gaagctggac	agaggccggt	ggaagaattt	4560

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Fig. 1 (continued)

gagctgtgcc	ttcccgacgg	ggatgtatct	attcatgggtg	ccgttgggtgc	ttccgaactc	4620
gcaaatacag	ccaaagcaga	tgtcccatac	atactgaaga	tggaatctca	cccgcacacc	4680
acctgctggc	ccgggagaac	cctctacttg	ctagctccca	gcttccctga	caaacagcgc	4740
tgggtcaccg	ccttagaatc	agttgtcgca	ggtagggagag	tttctaggga	aaaagcagaa	4800
gctgatgcta	aactgcttgg	aaactccctg	ctgaaactgg	aaggatgatga	ccgtctagac	4860
atgaactgca	cgctgcctt	cagtgaccag	gtggtgttgg	tgggcaccga	ggaagggctc	4920
tacgccctga	atgtcttgaa	aaactcccta	acccatgtcc	caggaattgg	agcagtcttc	4980
caaatttata	ttatcaagga	cctggagaag	ctactcatga	tagcaggaga	agagcgggca	5040
ctgtgtcttg	tggacgtgaa	gaaagtgaaa	cagtccctgg	cccagtccca	cctgcctgcc	5100
cagcccgaca	tctcacccaa	cattttttgaa	gctgtcaagg	gctgccactt	gtttggggca	5160
ggcaagattg	agaacgggct	ctgcatctgt	gcagccatgc	ccagcaaagt	cgctattctc	5220
cgctacaacg	aaaacctcag	caaatactgc	atccggaaaag	agatagagac	ctcagagccc	5280
tgcagctgta	tccacttcac	caattacagt	atcctcattg	gaaccaataa	attctacgaa	5340
atcgacatga	agcagtacac	gctcgaggaa	ttcctggata	agaatgacca	ttccttggca	5400
cctgctgtgt	ttgccgcctc	ttccaacagc	ttccctgtct	caatcgtgca	ggtgaacagc	5460
gcagggcagc	gagaggagta	cttgctgtgt	ttccacgaat	ttggagtgtt	cgtggattct	5520
tacggaagac	gtagccgcac	agacgatctc	aagtggagtc	gcttaccttt	ggcctttgcc	5580
tacagagaac	cctatctgtt	tgtgaccac	ttcaactcac	tcgaagtaat	tgagatccag	5640
gcacgctcct	cagcaggac	ccctgcccga	gcgtacctgg	acatcccga	cccgcgctac	5700
ctgggcccctg	ccatttcctc	aggagcgatt	tacttggcgt	cctcatacca	ggataaatta	5760
agggtcattt	gctgcaagg	aaacctcgtg	aaggagtccg	gcactgaaca	ccaccggggc	5820
ccgtccacct	ccgcgagcag	ccccaaacaag	cgaggcccac	ccacgtacaa	cgagcacatc	5880
accaagcgcg	tggcctccag	cccagcgccg	cccgaaggcc	ccagccacc	gcgagagcca	5940
agcacacccc	accgctaccg	cgagggggcg	accgagctgc	gcagggacaa	gtctcctggc	6000
cgccccctgg	agcgagagaa	gtcccccg	cggatgctca	gcacgcggag	agagcggctc	6060
cccgggaggc	tgtttgaaga	cagcagcagg	ggccggctgc	ctgcgggagc	cgtgaggacc	6120
ccgctgtccc	aggtgaacaa	ggtctgggac	cagtcttcag	tataa		6165

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Fig. 2

Met	Leu	Lys	Phe	Lys	Tyr	Gly	Ala	Arg	Asn	Pro	Leu	Asp	Ala	Gly	Ala
1				5					10					15	
Ala	Glu	Pro	Ile	Ala	Ser	Arg	Ala	Ser	Arg	Leu	Asn	Leu	Phe	Phe	Gln
			20					25					30		
Gly	Lys	Pro	Pro	Phe	Met	Thr	Gln	Gln	Gln	Met	Ser	Pro	Leu	Ser	Arg
		35					40				45				
Glu	Gly	Ile	Leu	Asp	Ala	Leu	Phe	Val	Leu	Phe	Glu	Glu	Cys	Ser	Gln
	50					55					60				
Pro	Ala	Leu	Met	Lys	Ile	Lys	His	Val	Ser	Asn	Phe	Val	Arg	Lys	Tyr
65				70						75				80	
Ser	Asp	Thr	Ile	Ala	Glu	Leu	Gln	Glu	Leu	Gln	Pro	Ser	Ala	Lys	Asp
			85						90					95	
Phe	Glu	Val	Arg	Ser	Leu	Val	Gly	Cys	Gly	His	Phe	Ala	Glu	Val	Gln
			100					105					110		
Val	Val	Arg	Glu	Lys	Ala	Thr	Gly	Asp	Ile	Tyr	Ala	Met	Lys	Val	Met
		115					120					125			
Lys	Lys	Lys	Ala	Leu	Leu	Ala	Gln	Glu	Gln	Val	Ser	Phe	Phe	Glu	Glu
	130					135					140				
Glu	Arg	Asn	Ile	Leu	Ser	Arg	Ser	Thr	Ser	Pro	Trp	Ile	Pro	Gln	Leu
145				150						155				160	
Gln	Tyr	Ala	Phe	Gln	Asp	Lys	Asn	His	Leu	Tyr	Leu	Val	Met	Glu	Tyr
			165						170					175	
Gln	Pro	Gly	Gly	Asp	Leu	Leu	Ser	Leu	Leu	Asn	Arg	Tyr	Glu	Asp	Gln
			180					185					190		
Leu	Asp	Glu	Asn	Leu	Ile	Gln	Phe	Tyr	Leu	Ala	Glu	Leu	Ile	Leu	Ala
	195					200					205				
Val	His	Ser	Val	His	Leu	Met	Gly	Tyr	Val	His	Arg	Asp	Ile	Lys	Pro
	210				215					220					
Glu	Asn	Ile	Leu	Val	Asp	Arg	Thr	Gly	His	Ile	Lys	Leu	Val	Asp	Phe
225				230						235				240	
Gly	Ser	Ala	Ala	Lys	Met	Asn	Ser	Asn	Lys	Met	Val	Asn	Ala	Lys	Leu
			245						250					255	
Pro	Ile	Gly	Thr	Pro	Asp	Tyr	Met	Ala	Pro	Glu	Val	Leu	Thr	Val	Met
			260					265					270		
Asn	Gly	Asp	Gly	Lys	Gly	Thr	Tyr	Gly	Leu	Asp	Cys	Asp	Trp	Trp	Ser
		275					280					285			
Val	Gly	Val	Ile	Ala	Tyr	Glu	Met	Ile	Tyr	Gly	Arg	Ser	Pro	Phe	Ala
	290					295					300				

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Fig. 2 (continued)

Glu	Gly	Thr	Ser	Ala	Arg	Thr	Phe	Asn	Asn	Ile	Met	Asn	Phe	Gln	Arg
305					310					315					320
Phe	Leu	Lys	Phe	Pro	Asp	Asp	Pro	Lys	Val	Ser	Ser	Asp	Phe	Leu	Asp
				325					330					335	
Leu	Ile	Gln	Ser	Leu	Leu	Cys	Gly	Gln	Lys	Glu	Arg	Leu	Lys	Phe	Glu
				340				345					350		
Gly	Leu	Cys	Cys	His	Pro	Phe	Phe	Ser	Lys	Ile	Asp	Trp	Asn	Asn	Ile
		355					360					365			
-Arg	Asn	Ser	Pro	Pro	Pro	Phe	Val	Pro	Thr	Leu	Lys	Ser	Asp	Asp	Asp
	370					375					380				
Thr	Ser	Asn	Phe	Asp	Glu	Pro	Glu	Lys	Asn	Ser	Trp	Val	Ser	Ser	Ser
385					390					395					400
Pro	Cys	Gln	Leu	Ser	Pro	Ser	Gly	Phe	Ser	Gly	Glu	Glu	Leu	Pro	Phe
				405						410				415	
Val	Gly	Phe	Ser	Tyr	Ser	Lys	Ala	Leu	Gly	Ile	Leu	Gly	Arg	Ser	Glu
			420					425					430		
Ser	Val	Val	Ser	Gly	Leu	Asp	Ser	Pro	Ala	Lys	Thr	Ser	Ser	Met	Glu
		435					440					445			
Lys	Lys	Leu	Leu	Ile	Lys	Ser	Lys	Glu	Leu	Gln	Asp	Ser	Gln	Asp	Lys
	450					455					460				
Cys	His	Lys	Met	Glu	Gln	Glu	Met	Thr	Arg	Leu	His	Arg	Arg	Val	Ser
465					470					475					480
Glu	Val	Glu	Ala	Val	Leu	Ser	Gln	Lys	Glu	Val	Glu	Leu	Lys	Ala	Ser
				485						490				495	
Glu	Thr	Gln	Arg	Ser	Leu	Leu	Glu	Gln	Asp	Leu	Ala	Thr	Tyr	Ile	Thr
			500					505					510		
Glu	Cys	Ser	Ser	Leu	Lys	Arg	Ser	Leu	Glu	Gln	Ala	Arg	Met	Glu	Val
		515					520					525			
Ser	Gln	Glu	Asp	Asp	Lys	Ala	Leu	Gln	Leu	Leu	His	Asp	Ile	Arg	Glu
	530					535					540				
Gln	Ser	Arg	Lys	Leu	Gln	Glu	Ile	Lys	Glu	Gln	Glu	Tyr	Gln	Ala	Gln
545					550					555					560
Val	Glu	Glu	Met	Arg	Leu	Met	Met	Asn	Gln	Leu	Glu	Glu	Asp	Leu	Val
				565						570				575	
Ser	Ala	Arg	Arg	Arg	Ser	Asp	Leu	Tyr	Glu	Ser	Glu	Leu	Arg	Glu	Ser
		580						585					590		
Arg	Leu	Ala	Ala	Glu	Glu	Phe	Lys	Arg	Lys	Ala	Thr	Glu	Cys	Gln	His
		595					600						605		

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Fig. 2 (continued)

Lys	Leu	Leu	Lys	Ala	Lys	Asp	Gln	Gly	Lys	Pro	Glu	Val	Gly	Glu	Tyr
610						615					620				
Ala	Lys	Leu	Glu	Lys	Ile	Asn	Ala	Glu	Gln	Gln	Leu	Lys	Ile	Gln	Glu
625					630					635					640
Leu	Gln	Glu	Lys	Leu	Glu	Lys	Ala	Val	Lys	Ala	Ser	Thr	Glu	Ala	Thr
				645					650					655	
Glu	Leu	Leu	Gln	Asn	Ile	Arg	Gln	Ala	Lys	Glu	Arg	Ala	Glu	Arg	Glu
				660				665					670		
Leu	Glu	Lys	Leu	Gln	Asn	Arg	Glu	Asp	Ser	Ser	Glu	Gly	Ile	Arg	Lys
		675					680					685			
Lys	Leu	Val	Glu	Ala	Glu	Glu	Arg	Arg	His	Ser	Leu	Glu	Asn	Lys	Val
690						695					700				
Lys	Arg	Leu	Glu	Thr	Met	Glu	Arg	Arg	Glu	Asn	Arg	Leu	Lys	Asp	Asp
705					710					715					720
Ile	Gln	Thr	Lys	Ser	Gln	Gln	Ile	Gln	Gln	Met	Ala	Asp	Lys	Ile	Leu
				725					730					735	
Glu	Leu	Glu	Glu	Lys	His	Arg	Glu	Ala	Gln	Val	Ser	Ala	Gln	His	Leu
				740				745					750		
Glu	Val	His	Leu	Lys	Gln	Lys	Glu	Gln	His	Tyr	Glu	Glu	Lys	Ile	Lys
		755					760					765			
Val	Leu	Asp	Asn	Gln	Ile	Lys	Lys	Asp	Leu	Ala	Asp	Lys	Glu	Thr	Leu
770						775						780			
Glu	Asn	Met	Met	Gln	Arg	His	Glu	Glu	Glu	Ala	His	Glu	Lys	Gly	Lys
785					790					795					800
Ile	Leu	Ser	Glu	Gln	Lys	Ala	Met	Ile	Asn	Ala	Met	Asp	Ser	Lys	Ile
				805					810					815	
Arg	Ser	Leu	Glu	Gln	Arg	Ile	Val	Glu	Leu	Ser	Glu	Ala	Asn	Lys	Leu
			820					825					830		
Ala	Ala	Asn	Ser	Ser	Leu	Phe	Thr	Gln	Arg	Asn	Met	Lys	Ala	Gln	Glu
		835					840					845			
Glu	Met	Ile	Ser	Glu	Leu	Arg	Gln	Gln	Lys	Phe	Tyr	Leu	Glu	Thr	Gln
		850				855					860				
Ala	Gly	Lys	Leu	Glu	Ala	Gln	Asn	Arg	Lys	Leu	Glu	Glu	Gln	Leu	Glu
865					870					875					880
Lys	Ile	Ser	His	Gln	Asp	His	Ser	Asp	Lys	Asn	Arg	Leu	Leu	Glu	Leu
				885					890					895	

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Fig. 2 (continued)

Glu Thr Arg Leu Arg Glu Val Ser Leu Glu His Glu Glu Gln Lys Leu	900	905	910
Glu Leu Lys Arg Gln Leu Thr Glu Leu Gln Leu Ser Leu Gln Glu Arg	915	920	925
Glu Ser Gln Leu Thr Ala Leu Gln Ala Ala Arg Ala Ala Leu Glu Ser	930	935	940
Gln Leu Arg Gln Ala Lys Thr Glu Leu Glu Glu Thr Thr Ala Glu Ala	945	950	955
Glu Glu Glu Ile Gln Ala Leu Thr Ala His Arg Asp Glu Ile Gln Arg	965	970	975
Lys Phe Asp Ala Leu Arg Asn Ser Cys Thr Val Ile Thr Asp Leu Glu	980	985	990
Glu Gln Leu Asn Gln Leu Thr Glu Asp Asn Ala Glu Leu Asn Asn Gln	995	1000	1005
Asn Phe Tyr Leu Ser Lys Gln Leu Asp Glu Ala Ser Gly Ala Asn Asp	1010	1015	1020
Glu Ile Val Gln Leu Arg Ser Glu Val Asp His Leu Arg Arg Glu Ile	1025	1030	1035
Thr Glu Arg Glu Met Gln Leu Thr Ser Gln Lys Gln Thr Met Glu Ala	1045	1050	1055
Leu Lys Thr Thr Cys Thr Met Leu Glu Glu Gln Val Met Asp Leu Glu	1060	1065	1070
Ala Leu Asn Asp Glu Leu Leu Glu Lys Glu Arg Gln Trp Glu Ala Trp	1075	1080	1085
Arg Ser Val Leu Gly Asp Glu Lys Ser Gln Phe Glu Cys Arg Val Arg	1090	1095	1100
Glu Leu Gln Arg Met Leu Asp Thr Glu Lys Gln Ser Arg Ala Arg Ala	1105	1110	1115
Asp Gln Arg Ile Thr Glu Ser Arg Gln Val Val Glu Leu Ala Val Lys	1125	1130	1135
Glu His Lys Ala Glu Ile Leu Ala Leu Gln Gln Ala Leu Lys Glu Gln	1140	1145	1150
Lys Leu Lys Ala Glu Ser Leu Ser Asp Lys Leu Asn Asp Leu Glu Lys	1155	1160	1165
Lys His Ala Met Leu Glu Met Asn Ala Arg Ser Leu Gln Gln Lys Leu	1170	1175	1180
Glu Thr Glu Arg Glu Leu Lys Gln Arg Leu Leu Glu Glu Gln Ala Lys	1185	1190	1195
			1200

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Fig. 2 (continued)

Leu	Gln	Gln	Gln	Met	Asp	Leu	Gln	Lys	Asn	His	Ile	Phe	Arg	Leu	Thr			
				1205					1210					1215				
Gln	Gly	Leu	Gln	Glu	Ala	Leu	Asp	Arg	Ala	Asp	Leu	Leu	Lys	Thr	Glu			
				1220				1225					1230					
Arg	Ser	Asp	Leu	Glu	Tyr	Gln	Leu	Glu	Asn	Ile	Gln	Val	Leu	Tyr	Ser			
				1235				1240					1245					
His	Glu	Lys	Val	Lys	Met	Glu	Gly	Thr	Ile	Ser	Gln	Gln	Thr	Lys	Leu			
				1250				1255				1260						
Ile	Asp	Phe	Leu	Gln	Ala	Lys	Met	Asp	Gln	Pro	Ala	Lys	Lys	Lys	Lys			
1265					1270				1275						1280			
Val	Pro	Leu	Gln	Tyr	Asn	Glu	Leu	Lys	Leu	Ala	Leu	Glu	Lys	Glu	Lys			
				1285				1290					1295					
Ala	Arg	Cys	Ala	Glu	Leu	Glu	Glu	Ala	Leu	Gln	Lys	Thr	Arg	Ile	Glu			
				1300				1305					1310					
Leu	Arg	Ser	Ala	Arg	Glu	Glu	Ala	Ala	His	Arg	Lys	Ala	Thr	Asp	His			
				1315				1320					1325					
Pro	His	Pro	Ser	Thr	Pro	Ala	Thr	Ala	Arg	Gln	Gln	Ile	Ala	Met	Ser			
				1330				1335				1340						
Ala	Ile	Val	Arg	Ser	Pro	Glu	His	Gln	Pro	Ser	Ala	Met	Ser	Leu	Leu			
1345					1350				1355					1360				
Ala	Pro	Pro	Ser	Ser	Arg	Arg	Lys	Glu	Ser	Ser	Thr	Pro	Glu	Glu	Phe			
				1365				1370					1375					
Ser	Arg	Arg	Leu	Lys	Glu	Arg	Met	His	His	Asn	Ile	Pro	His	Arg	Phe			
				1380				1385					1390					
Asn	Val	Gly	Leu	Asn	Met	Arg	Ala	Thr	Lys	Cys	Ala	Val	Cys	Leu	Asp			
				1395				1400				1405						
Thr	Val	His	Phe	Gly	Arg	Gln	Ala	Ser	Lys	Cys	Leu	Glu	Cys	Gln	Val			
				1410				1415				1420						
Met	Cys	His	Pro	Lys	Cys	Ser	Thr	Cys	Leu	Pro	Ala	Thr	Cys	Gly	Leu			
1425					1430				1435					1440				
Pro	Ala	Glu	Tyr	Ala	Thr	His	Phe	Thr	Glu	Ala	Phe	Cys	Arg	Asp	Lys			
				1445				1450					1455					
Met	Asn	Ser	Pro	Gly	Leu	Gln	Thr	Lys	Glu	Pro	Ser	Ser	Ser	Leu	His			
				1460				1465					1470					
Leu	Glu	Gly	Trp	Met	Lys	Val	Pro	Arg	Asn	Asn	Lys	Arg	Gly	Gln	Gln			
				1475				1480					1485					

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Fig. 2 (continued)

Gly Trp Asp Arg Lys Tyr Ile Val Leu Glu Gly Ser Lys Val Leu Ile			
1490	1495	1500	
Tyr Asp Asn Glu Ala Arg Glu Ala Gly Gln Arg Pro Val Glu Glu Phe			
1505	1510	1515	1520
Glu Leu Cys Leu Pro Asp Gly Asp Val Ser Ile His Gly Ala Val Gly			
	1525	1530	1535
Ala Ser Glu Leu Ala Asn Thr Ala Lys Ala Asp Val Pro Tyr Ile Leu			
	1540	1545	1550
Lys Met Glu Ser His Pro His Thr Thr Cys Trp Pro Gly Arg Thr Leu			
	1555	1560	1565
Tyr Leu Leu Ala Pro Ser Phe Pro Asp Lys Gln Arg Trp Val Thr Ala			
1570	1575	1580	
Leu Glu Ser Val Val Ala Gly Gly Arg Val Ser Arg Glu Lys Ala Glu			
1585	1590	1595	1600
Ala Asp Ala Lys Leu Leu Gly Asn Ser Leu Leu Lys Leu Glu Gly Asp			
	1605	1610	1615
Asp Arg Leu Asp Met Asn Cys Thr Leu Pro Phe Ser Asp Gln Val Val			
	1620	1625	1630
Leu Val Gly Thr Glu Glu Gly Leu Tyr Ala Leu Asn Val Leu Lys Asn			
	1635	1640	1645
Ser Leu Thr His Val Pro Gly Ile Gly Ala Val Phe Gln Ile Tyr Ile			
1650	1655	1660	
Ile Lys Asp Leu Glu Lys Leu Leu Met Ile Ala Gly Glu Glu Arg Ala			
1665	1670	1675	1680
Leu Cys Leu Val Asp Val Lys Lys Val Lys Gln Ser Leu Ala Gln Ser			
	1685	1690	1695
His Leu Pro Ala Gln Pro Asp Ile Ser Pro Asn Ile Phe Glu Ala Val			
	1700	1705	1710
Lys Gly Cys His Leu Phe Gly Ala Gly Lys Ile Glu Asn Gly Leu Cys			
	1715	1720	1725
Ile Cys Ala Ala Met Pro Ser Lys Val Val Ile Leu Arg Tyr Asn Glu			
1730	1735	1740	
Asn Leu Ser Lys Tyr Cys Ile Arg Lys Glu Ile Glu Thr Ser Glu Pro			
1745	1750	1755	1760
Cys Ser Cys Ile His Phe Thr Asn Tyr Ser Ile Leu Ile Gly Thr Asn			
	1765	1770	1775

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Fig. 2 (continued)

Lys	Phe	Tyr	Glu	Ile	Asp	Met	Lys	Gln	Tyr	Thr	Leu	Glu	Glu	Phe	Leu	1780	1785	1790
Asp	Lys	Asn	Asp	His	Ser	Leu	Ala	Pro	Ala	Val	Phe	Ala	Ala	Ser	Ser	1795	1800	1805
Asn	Ser	Phe	Pro	Val	Ser	Ile	Val	Gln	Val	Asn	Ser	Ala	Gly	Gln	Arg	1810	1815	1820
Glu	Glu	Tyr	Leu	Leu	Cys	Phe	His	Glu	Phe	Gly	Val	Phe	Val	Asp	Ser	1825	1830	1835
Tyr	Gly	Arg	Arg	Ser	Arg	Thr	Asp	Asp	Leu	Lys	Trp	Ser	Arg	Leu	Pro	1845	1850	1855
Leu	Ala	Phe	Ala	Tyr	Arg	Glu	Pro	Tyr	Leu	Phe	Val	Thr	His	Phe	Asn	1860	1865	1870
Ser	Leu	Glu	Val	Ile	Glu	Ile	Gln	Ala	Arg	Ser	Ser	Ala	Gly	Thr	Pro	1875	1880	1885
Ala	Arg	Ala	Tyr	Leu	Asp	Ile	Pro	Asn	Pro	Arg	Tyr	Leu	Gly	Pro	Ala	1890	1895	1900
Ile	Ser	Ser	Gly	Ala	Ile	Tyr	Leu	Ala	Ser	Ser	Tyr	Gln	Asp	Lys	Leu	1905	1910	1915
Arg	Val	Ile	Cys	Cys	Lys	Gly	Asn	Leu	Val	Lys	Glu	Ser	Gly	Thr	Glu	1925	1930	1935
His	His	Arg	Gly	Pro	Ser	Thr	Ser	Arg	Ser	Ser	Pro	Asn	Lys	Arg	Gly	1940	1945	1950
Pro	Pro	Thr	Tyr	Asn	Glu	His	Ile	Thr	Lys	Arg	Val	Ala	Ser	Ser	Pro	1955	1960	1965
Ala	Pro	Pro	Glu	Gly	Pro	Ser	His	Pro	Arg	Glu	Pro	Ser	Thr	Pro	His	1970	1975	1980
Arg	Tyr	Arg	Glu	Gly	Arg	Thr	Glu	Leu	Arg	Arg	Asp	Lys	Ser	Pro	Gly	1985	1990	1995
Arg	Pro	Leu	Glu	Arg	Glu	Lys	Ser	Pro	Gly	Arg	Met	Leu	Ser	Thr	Arg	2005	2010	2015
Arg	Glu	Arg	Ser	Pro	Gly	Arg	Leu	Phe	Glu	Asp	Ser	Ser	Arg	Gly	Arg	2020	2025	2030
Leu	Pro	Ala	Gly	Ala	Val	Arg	Thr	Pro	Leu	Ser	Gln	Val	Asn	Lys	Val	2035	2040	2045
Trp	Asp	Gln	Ser	Ser	Val											2050		

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Fig. 3

Met	Leu	Lys	Phe	Lys	Tyr	Gly	Val	Arg	Asn	Pro	Pro	Glu	Ala	Ser	Ala
1				5					10					15	
Ser	Glu	Pro	Ile	Ala	Ser	Arg	Ala	Ser	Arg	Leu	Asn	Leu	Phe	Phe	Gln
			20					25					30		
Gly	Lys	Pro	Pro	Leu	Met	Thr	Gln	Gln	Gln	Met	Ser	Ala	Leu	Ser	Arg
		35					40					45			
Glu	Gly	Met	Leu	Asp	Ala	Leu	Phe	Ala	Leu	Phe	Glu	Glu	Cys	Ser	Gln
	50					55				60					
Pro	Ala	Leu	Met	Lys	Met	Lys	His	Val	Ser	Ser	Phe	Val	Gln	Lys	Tyr
65				70						75				80	
Ser	Asp	Thr	Ile	Ala	Glu	Leu	Arg	Glu	Leu	Gln	Pro	Ser	Ala	Arg	Asp
			85					90					95		
Phe	Glu	Val	Arg	Ser	Leu	Val	Gly	Cys	Gly	His	Phe	Ala	Glu	Val	Gln
			100				105					110			
Val	Val	Arg	Glu	Lys	Ala	Thr	Gly	Asp	Val	Tyr	Ala	Met	Lys	Ile	Met
		115					120					125			
Lys	Lys	Lys	Ala	Leu	Leu	Ala	Gln	Glu	Gln	Val	Ser	Phe	Phe	Glu	Glu
	130					135				140					
Glu	Arg	Asn	Ile	Leu	Ser	Arg	Ser	Thr	Ser	Pro	Trp	Ile	Pro	Gln	Leu
145				150						155				160	
Gln	Tyr	Ala	Phe	Gln	Asp	Lys	Asn	Asn	Leu	Tyr	Leu	Val	Met	Glu	Tyr
			165					170					175		
Gln	Pro	Gly	Gly	Asp	Phe	Leu	Ser	Leu	Leu	Asn	Arg	Tyr	Glu	Asp	Gln
			180					185				190			
Leu	Asp	Glu	Ser	Met	Ile	Gln	Phe	Tyr	Leu	Ala	Glu	Leu	Ile	Leu	Ala
	195						200				205				
Val	His	Ser	Val	His	Gln	Met	Gly	Tyr	Val	His	Arg	Asp	Ile	Lys	Pro
	210					215					220				
Glu	Asn	Ile	Leu	Ile	Asp	Arg	Thr	Gly	Glu	Ile	Lys	Leu	Val	Asp	Phe
225				230						235				240	
Gly	Ser	Ala	Ala	Lys	Met	Asn	Ser	Asn	Lys	Val	Asp	Ala	Lys	Leu	Pro
			245					250				255			
Ile	Gly	Thr	Pro	Asp	Tyr	Met	Ala	Pro	Glu	Val	Leu	Thr	Val	Met	Asn
			260					265				270			
Glu	Asp	Arg	Arg	Gly	Thr	Tyr	Gly	Leu	Asp	Cys	Asp	Trp	Trp	Ser	Val
	275						280				285				
Gly	Val	Val	Ala	Tyr	Glu	Met	Val	Tyr	Gly	Lys	Thr	Pro	Phe	Thr	Glu
	290					295					300				

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Fig. 3 (continued)

Gly	Thr	Ser	Ala	Arg	Thr	Phe	Asn	Asn	Ile	Met	Asn	Phe	Gln	Arg	Phe	305	310	315	320
Leu	Lys	Phe	Pro	Asp	Asp	Pro	Lys	Val	Ser	Ser	Glu	Leu	Leu	Asp	Leu	325	330	335	
Leu	Gln	Ser	Leu	Leu	Cys	Val	Gln	Lys	Glu	Arg	Leu	Lys	Phe	Glu	Gly	340	345	350	
Leu	Cys	Cys	His	Pro	Phe	Phe	Ala	Arg	Thr	Asp	Trp	Asn	Asn	Ile	Arg	355	360	365	
Asn	Ser	Pro	Pro	Pro	Phe	Val	Pro	Thr	Leu	Lys	Ser	Asp	Asp	Asp	Thr	370	375	380	
Ser	Asn	Phe	Asp	Glu	Pro	Glu	Lys	Asn	Ser	Trp	Ala	Phe	Ile	Leu	Cys	385	390	395	400
Val	Pro	Ala	Glu	Pro	Leu	Ala	Phe	Ser	Gly	Glu	Glu	Leu	Pro	Phe	Val	405	410	415	
Gly	Phe	Ser	Tyr	Ser	Lys	Ala	Leu	Gly	Tyr	Leu	Gly	Arg	Ser	Glu	Ser	420	425	430	
Val	Val	Ser	Ser	Leu	Asp	Ser	Pro	Ala	Lys	Val	Ser	Ser	Met	Glu	Lys	435	440	445	
Lys	Leu	Leu	Ile	Lys	Ser	Lys	Glu	Leu	Gln	Asp	Ser	Gln	Asp	Lys	Cys	450	455	460	
His	Lys	Met	Glu	Gln	Glu	Met	Thr	Arg	Leu	His	Arg	Arg	Val	Ser	Glu	465	470	475	480
Val	Glu	Ala	Val	Leu	Ser	Gln	Lys	Glu	Val	Glu	Leu	Lys	Ala	Ser	Glu	485	490	495	
Thr	Gln	Arg	Ser	Leu	Leu	Glu	Gln	Asp	Leu	Ala	Thr	Tyr	Ile	Thr	Glu	500	505	510	
Cys	Ser	Ser	Leu	Lys	Arg	Ser	Leu	Glu	Gln	Ala	Arg	Met	Glu	Val	Ser	515	520	525	
Gln	Glu	Asp	Asp	Lys	Ala	Leu	Gln	Leu	Leu	His	Asp	Ile	Arg	Glu	Gln	530	535	540	
Ser	Arg	Lys	Leu	Gln	Glu	Ile	Lys	Glu	Gln	Glu	Tyr	Gln	Ala	Gln	Val	545	550	555	560
Glu	Glu	Met	Arg	Leu	Met	Met	Asn	Gln	Leu	Glu	Glu	Asp	Leu	Val	Ser	565	570	575	
Ala	Arg	Arg	Arg	Ser	Asp	Leu	Tyr	Glu	Ser	Glu	Leu	Arg	Glu	Ser	Arg	580	585	590	

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Fig. 3 (continued)

Leu	Ala	Ala	Glu	Glu	Phe	Lys	Arg	Lys	Ala	Asn	Glu	Cys	Gln	His	Lys
	595						600					605			
Leu	Met	Lys	Ala	Lys	Asp	Gln	Gly	Lys	Pro	Glu	Val	Gly	Glu	Tyr	Ser
	610						615					620			
Lys	Leu	Glu	Lys	Ile	Asn	Ala	Glu	Gln	Gln	Leu	Lys	Ile	Gln	Glu	Leu
625						630					635				640
Gln	Glu	Lys	Leu	Glu	Lys	Ala	Val	Lys	Ala	Ser	Thr	Glu	Ala	Thr	Glu
						645				650					655
Leu	Leu	Gln	Asn	Ile	Arg	Gln	Ala	Lys	Glu	Arg	Ala	Glu	Arg	Glu	Leu
						660				665					670
Glu	Lys	Leu	His	Asn	Arg	Glu	Asp	Ser	Ser	Glu	Gly	Ile	Lys	Lys	Lys
						675				680					685
Leu	Val	Glu	Ala	Glu	Glu	Arg	Arg	His	Ser	Leu	Glu	Asn	Lys	Val	Lys
						690				695					700
Arg	Leu	Glu	Thr	Met	Glu	Arg	Arg	Glu	Asn	Arg	Leu	Lys	Asp	Asp	Ile
705						710				715					720
Gln	Thr	Lys	Ser	Glu	Gln	Ile	Gln	Gln	Met	Ala	Asp	Lys	Ile	Leu	Glu
						725				730					735
Leu	Glu	Glu	Lys	His	Arg	Glu	Ala	Gln	Val	Ser	Ala	Gln	His	Leu	Glu
						740				745					750
Val	His	Leu	Lys	Gln	Lys	Glu	Gln	His	Tyr	Glu	Glu	Lys	Ile	Lys	Val
						755				760					765
Leu	Asp	Asn	Gln	Ile	Lys	Lys	Asp	Leu	Ala	Asp	Lys	Glu	Ser	Leu	Glu
						770				775					780
Asn	Met	Met	Gln	Arg	His	Glu	Glu	Glu	Ala	His	Glu	Lys	Gly	Lys	Ile
785						790				795					800
Leu	Ser	Glu	Gln	Lys	Ala	Met	Ile	Asn	Ala	Met	Asp	Ser	Lys	Ile	Arg
						805				810					815
Ser	Leu	Glu	Gln	Arg	Ile	Val	Glu	Leu	Ser	Glu	Ala	Asn	Lys	Leu	Ala
						820				825					830
Ala	Asn	Ser	Ser	Leu	Phe	Thr	Gln	Arg	Asn	Met	Lys	Ala	Gln	Glu	Glu
						835				840					845
Met	Ile	Ser	Glu	Leu	Arg	Gln	Gln	Lys	Phe	Tyr	Leu	Glu	Thr	Gln	Ala
						850				855					860
Gly	Lys	Leu	Glu	Ala	Gln	Asn	Arg	Lys	Leu	Glu	Glu	Gln	Leu	Glu	Lys
865						870				875					880
Ile	Ser	His	Gln	Asp	His	Ser	Asp	Lys	Ser	Arg	Leu	Leu	Glu	Leu	Glu
						885				890					895

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Fig. 3 (continued)

Thr	Arg	Leu	Arg	Glu	Val	Ser	Leu	Glu	His	Glu	Gln	Lys	Leu	Glu		
			900					905				910				
Leu	Lys	Arg	Gln	Leu	Thr	Glu	Leu	Gln	Leu	Ser	Leu	Gln	Glu	Arg	Glu	
			915					920				925				
Ser	Gln	Leu	Thr	Ala	Leu	Gln	Ala	Ala	Arg	Ala	Ala	Leu	Glu	Ser	Gln	
			930				935				940					
Leu	Arg	Gln	Ala	Lys	Thr	Glu	Leu	Glu	Glu	Thr	Thr	Ala	Glu	Ala	Glu	
945						950				955					960	
Glu	Glu	Ile	Gln	Ala	Leu	Thr	Ala	His	Arg	Asp	Glu	Ile	Gln	Arg	Lys	
			965					970					975			
Phe	Asp	Ala	Leu	Arg	Asn	Ser	Cys	Thr	Val	Ile	Thr	Asp	Leu	Glu	Glu	
			980					985				990				
Gln	Leu	Asn	Gln	Leu	Thr	Glu	Asp	Asn	Ala	Glu	Leu	Asn	Asn	Gln	Asn	
			995				1000					1005				
Phe	Tyr	Leu	Ser	Lys	Gln	Leu	Asp	Glu	Ala	Ser	Gly	Ala	Asn	Asp	Glu	
			1010				1015				1020					
Ile	Val	Gln	Leu	Arg	Ser	Glu	Val	Asp	His	Leu	Arg	Arg	Glu	Ile	Thr	
1025						1030				1035					1040	
Glu	Arg	Glu	Met	Gln	Leu	Thr	Ser	Gln	Lys	Gln	Thr	Met	Glu	Ala	Leu	
			1045					1050				1055				
Lys	Thr	Thr	Cys	Thr	Met	Leu	Glu	Glu	Gln	Val	Leu	Asp	Leu	Glu	Ala	
			1060					1065				1070				
Leu	Asn	Asp	Glu	Leu	Leu	Glu	Lys	Glu	Arg	Gln	Trp	Glu	Ala	Trp	Arg	
			1075				1080				1085					
Ser	Val	Leu	Gly	Asp	Glu	Lys	Ser	Gln	Phe	Glu	Cys	Arg	Val	Arg	Glu	
			1090				1095				1100					
Leu	Gln	Arg	Met	Leu	Asp	Thr	Glu	Lys	Gln	Ser	Arg	Ala	Arg	Ala	Asp	
1105						1110				1115					1120	
Gln	Arg	Ile	Thr	Glu	Ser	Arg	Gln	Val	Val	Glu	Leu	Ala	Val	Lys	Glu	
			1125					1130				1135				
His	Lys	Ala	Glu	Ile	Leu	Ala	Leu	Gln	Gln	Ala	Leu	Lys	Glu	Gln	Lys	
			1140					1145				1150				
Leu	Lys	Ala	Glu	Ser	Leu	Ser	Asp	Lys	Leu	Asn	Asp	Leu	Glu	Lys	Lys	
			1155				1160				1165					
His	Ala	Met	Leu	Glu	Met	Asn	Ala	Arg	Ser	Leu	Gln	Gln	Lys	Leu	Glu	
			1170				1175				1180					

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Fig. 3 (continued)

Thr Glu Arg Glu Leu Lys Gln Arg Leu Leu Glu Glu Gln Ala Lys Leu			
1185	1190	1195	1200
Gln Gln Gln Met Asp Leu Gln Lys Asn His Ile Phe Arg Leu Thr Gln			
	1205	1210	1215
Gly Leu Gln Glu Ala Leu Asp Arg Ala Asp Leu Leu Lys Thr Glu Arg			
	1220	1225	1230
Ser Asp Leu Glu Tyr Gln Leu Glu Asn Ile Gln Val Leu Tyr Ser His			
	1235	1240	1245
Glu Lys Val Lys Met Glu Gly Thr Ile Ser Gln Gln Thr Lys Leu Ile			
	1250	1255	1260
Asp Phe Leu Gln Ala Lys Met Asp Gln Pro Ala Lys Lys Lys Lys Val			
1265	1270	1275	1280
Pro Leu Gln Tyr Asn Glu Leu Lys Leu Ala Leu Glu Lys Glu Lys Ala			
	1285	1290	1295
Arg Cys Ala Glu Leu Glu Glu Ala Leu Gln Lys Thr Arg Ile Glu Leu			
	1300	1305	1310
Arg Ser Ala Arg Glu Glu Ala Ala His Arg Lys Ala Thr Asp His Pro			
	1315	1320	1325
His Pro Ser Thr Pro Ala Thr Ala Arg Gln Gln Ile Ala Met Ser Ala			
	1330	1335	1340
Ile Val Arg Ser Pro Glu His Gln Pro Ser Ala Met Ser Leu Leu Ala			
1345	1350	1355	1360
Pro Pro Ser Ser Arg Arg Lys Glu Ser Ser Thr Pro Glu Glu Phe Ser			
	1365	1370	1375
Arg Arg Leu Lys Glu Arg Met His His Asn Ile Pro His Arg Phe Asn			
	1380	1385	1390
Val Gly Leu Asn Met Arg Ala Thr Lys Cys Ala Val Cys Leu Asp Thr			
	1395	1400	1405
Val His Phe Gly Arg Gln Ala Ser Lys Cys Leu Glu Cys Gln Val Met			
	1410	1415	1420
Cys His Pro Lys Cys Ser Thr Cys Leu Pro Ala Thr Cys Gly Leu Pro			
1425	1430	1435	1440
Ala Glu Tyr Ala Thr His Phe Thr Glu Ala Phe Cys Arg Asp Lys Met			
	1445	1450	1455
Asn Ser Pro Gly Leu Gln Ser Lys Glu Pro Gly Ser Ser Leu His Leu			
	1460	1465	1470

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Fig. 3 (continued)

Glu Gly Trp Met Lys Val Pro Arg Asn Asn Lys Arg Gly Gln Gln Gly	1475	1480	1485
Trp Asp Arg Lys Tyr Ile Val Leu Glu Gly Ser Lys Val Leu Ile Tyr	1490	1495	1500
Asp Asn Glu Ala Arg Glu Ala Gly Gln Arg Pro Val Glu Glu Phe Glu	1505	1510	1515
Leu Cys Leu Pro Asp Gly Asp Val Ser Ile His Gly Ala Val Gly Ala	1525	1530	1535
Ser Glu Leu Ala Asn Thr Ala Lys Ala Asp Val Pro Tyr Ile Leu Lys	1540	1545	1550
Met Glu Ser His Pro His Thr Thr Cys Trp Pro Gly Arg Thr Leu Tyr	1555	1560	1565
Leu Leu Ala Pro Ser Phe Pro Asp Lys Gln Arg Trp Val Thr Ala Leu	1570	1575	1580
Glu Ser Val Val Ala Gly Gly Arg Val Ser Arg Glu Lys Ala Glu Ala	1585	1590	1595
Asp Ala Lys Leu Leu Gly Asn Ser Leu Leu Lys Leu Glu Gly Asp Asp	1605	1610	1615
Arg Leu Asp Met Asn Cys Thr Leu Pro Phe Ser Asp Gln Val Val Leu	1620	1625	1630
Val Gly Thr Glu Glu Gly Leu Tyr Ala Leu Asn Val Leu Lys Asn Ser	1635	1640	1645
Leu Thr His Ile Pro Gly Ile Gly Ala Val Phe Gln Ile Tyr Ile Ile	1650	1655	1660
Lys Asp Leu Glu Lys Leu Leu Met Ile Ala Gly Glu Glu Arg Ala Leu	1665	1670	1675
Cys Leu Val Asp Val Lys Lys Val Lys Gln Ser Leu Ala Gln Ser His	1685	1690	1695
Leu Pro Ala Gln Pro Asp Val Ser Pro Asn Ile Phe Glu Ala Val Lys	1700	1705	1710
Gly Cys His Leu Phe Ala Ala Gly Lys Ile Glu Asn Ser Leu Cys Ile	1715	1720	1725
Cys Ala Ala Met Pro Ser Lys Val Val Ile Leu Arg Tyr Asn Asp Asn	1730	1735	1740
Leu Ser Lys Tyr Cys Ile Arg Lys Glu Ile Glu Thr Ser Glu Pro Cys	1745	1750	1755
			1760

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Fig. 3 (continued)

Ser Cys Ile His Phe Thr Asn Tyr Ser Ile Leu Ile Gly Thr Asn Lys			
	1765	1770	1775
Phe Tyr Glu Ile Asp Met Lys Gln Tyr Thr Leu Asp Glu Phe Leu Asp			
	1780	1785	1790
Lys Asn Asp His Ser Leu Ala Pro Ala Val Phe Ala Ser Ser Ser Asn			
	1795	1800	1805
Ser Phe Pro Val Ser Ile Val Gln Ala Asn Ser Ala Gly Gln Arg Glu			
	1810	1815	1820
Glu Tyr Leu Leu Cys Phe His Glu Phe Gly Val Phe Val Asp Ser Tyr			
	1825	1830	1835
Gly Arg Arg Ser Arg Thr Asp Asp Leu Lys Trp Ser Arg Leu Pro Leu			
	1845	1850	1855
Ala Phe Ala Tyr Arg Glu Pro Tyr Leu Phe Val Thr His Phe Asn Ser			
	1860	1865	1870
Leu Glu Val Ile Glu Ile Gln Ala Arg Ser Ser Leu Gly Ser Pro Ala			
	1875	1880	1885
Arg Ala Tyr Leu Glu Ile Pro Asn Pro Arg Tyr Leu Gly Pro Ala Ile			
	1890	1895	1900
Ser Ser Gly Ala Ile Tyr Leu Ala Ser Ser Tyr Gln Asp Lys Leu Arg			
	1905	1910	1915
Val Ile Cys Cys Lys Gly Asn Leu Val Lys Glu Ser Gly Thr Glu Gln			
	1925	1930	1935
His Arg Val Pro Ser Thr Ser Arg Ser Ser Pro Asn Lys Arg Gly Pro			
	1940	1945	1950
Pro Thr Tyr Asn Glu His Ile Thr Lys Arg Val Ala Ser Ser Pro Ala			
	1955	1960	1965
Pro Pro Glu Gly Pro Ser His Pro Arg Glu Pro Ser Thr Pro His Arg			
	1970	1975	1980
Tyr Arg Asp Arg Glu Gly Arg Thr Glu Leu Arg Arg Asp Lys Ser Pro			
	1985	1990	1995
Gly Arg Pro Leu Glu Arg Glu Lys Ser Pro Gly Arg Met Leu Ser Thr			
	2005	2010	2015
Arg Arg Glu Arg Ser Pro Gly Arg Leu Phe Glu Asp Ser Ser Arg Gly			
	2020	2025	2030
Arg Leu Pro Ala Gly Ala Val Arg Thr Pro Leu Ser Gln Val Asn Lys			
	2035	2040	2045
Val Trp Asp Gln Ser Ser Val			
	2050	2055	

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Fig. 4

atgttgaagt	tcaaatatgg	agcgcggaat	cctttggatg	ctggtgctgc	tgaaccatt	60
gccagccggg	cctccaggct	gaatctgttc	ttccagggga	aaccaccctt	tatgactcaa	120
cagcagatgt	ctcctctttc	ccgagaaggg	atattagatg	ccctctttgt	tctctttgaa	180
gaatgcagtc	agcctgctct	gatgaagatt	aagcacgtga	gcaactttgt	ccggaagtat	240
tccgacacca	tagctgagtt	acaggagctc	cagccttcgg	caaaggactt	cgaagtcaga	300
agtcttgtag	gttgtggtca	ctttgctgaa	gtgcagggtg	taagagagaa	agcaaccggg	360
gacatctatg	ctatgaaagt	gatgaagaag	aaggctttat	tggcccagga	gcaggtttca	420
ttttttgagg	aagagcggaa	catattatct	cgaagcaca	gcccgtggat	cccccaatta	480
cagtatgcct	ttcaggacaa	aaatcacctt	tatctggtca	tggaatatca	gcctggaggg	540
gacttgctgt	cacttttgaa	tagatatgag	gaccagttag	atgaaaacct	gatacagttt	600
tacctagctg	agctgatttt	ggctgttcac	agcgttcac	tgatgggata	cgtgcatoga	660
gacatcaagc	ctgagaacat	tctcgttgac	cgcacaggac	acatcaagct	ggtggatttt	720
ggatctgccg	cgaaaatgaa	ttcaaacaag	atggtgaatg	ccaaactccc	gattgggacc	780
ccagattaca	tggctcctga	agtgtgact	gtgatgaacg	gggatggaaa	aggcacctac	840
ggcctggact	gtgactgggt	gtcagtgggc	gtgattgcct	atgagatgat	ttatgggaga	900
ttccccttcg	cagagggaac	ctctgccaga	accttcaata	acattatgaa	tttcagcgg	960
tttttgaaat	ttccagatga	ccccaaagtg	agcagtgact	ttcttgatct	gattcaaagc	1020
ttgttgctgcg	gccagaaaga	gagactgaag	tttgaaggct	tttgctgcca	tcctttcttc	1080
tctaaaattg	actggaacaa	cattcgtaac	tctcctcccc	ccttcgttcc	caccctcaag	1140
tctgacgatg	acacctccaa	ttttgatgaa	ccagagaaga	attcgtgggt	ttcatcctct	1200
ccgtgccagc	tgagcccctc	aggcttctcg	ggtgaagaac	tgccgtttgt	ggggttttcg	1260
tacagcaagg	cactggggat	tcttggtaga	tctgagtctg	ttgtgtcggg	tctggactcc	1320
cctgccaaga	ctagctccat	ggaaaagaaa	cttctcatca	aaagcaaaga	gctacaagac	1380
tctcaggaca	agtgtcacia	gatggagcag	gaaatgacct	ggttacatcg	gagagtgtca	1440
gaggtggagg	ctgtgcttag	tcagaaggag	gtggagctga	aggcctctga	gactcagaga	1500
ttcctcctgg	agcaggacct	tgctacctac	atcacagaat	gcagtagctt	aaagcgaagt	1560
ttggagcaag	cacggatgga	ggtgtcccag	gaggatgaca	aagcactgca	gcttctccat	1620
gatatcagag	agcagagccg	gaagctccaa	gaaatcaaag	agcaggagta	ccaggctcaa	1680
gtggaagaaa	tgaggttgat	gatgaatcag	ttggaagagg	atcttgtctc	agcaagaaga	1740
cggagtgate	tctacgaatc	tgagctgaga	gagtctcggc	ttgctgctga	agaattcaag	1800
cggaaagcga	cagaatgtca	gcataaactg	ttgaaggcta	aggatcaagg	gaagcctgaa	1860
gtggggagaat	atgcgaaact	ggagaagatc	aatgctgagc	agcagctcaa	aattcaggag	1920
ctccaagaga	aactggagaa	ggctgtaaaa	gccagcacgg	aggccaccga	gctgctgcag	1980
aatatccgcc	aggcaaagga	gcgagccgag	agggagctgg	agaagctgca	gaaccgagag	2040
gattcttctg	aaggcatcag	aaagaagctg	gtggaagctg	aggaacgccg	ccattctctg	2100
gagaacaagg	taaagagact	agagaccatg	gagcgtagag	aaaacagact	gaaggatgac	2160
atccagacaa	aatcccaaca	gatccagcag	atggctgata	aaattctgga	gctcgaagag	2220
aaacatcggg	aggcccaagt	ctcagcccag	cacctagaag	tgcacctgaa	acagaaagag	2280

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Fig. 4 (continued)

cagcactatg	aggaaaagat	taaagtgttg	gacaatcaga	taaagaaaga	cctggctgac	2340
aaggagacac	tggagaacat	gatgcagaga	cacgaggagg	aggcccatga	gaagggcaaa	2400
attctcagcg	aacagaaggc	gatgatcaat	gctatggatt	ccaagatcag	atccctggaa	2460
cagaggattg	tggaactgtc	tgaagccaat	aaacttgacg	caaatagcag	tctttttacc	2520
caaaggaaca	tgaaggccca	agaagagatg	atctctgaac	tcaggcaaca	gaaattttac	2580
ctggagacac	aggctgggaa	gttggaggcc	cagaaccgaa	aactggagga	gcagctggag	2640
aagatcagcc	accaagacca	cagtgcacaag	aatcggctgc	tggaaactgga	gacaagattg	2700
cgggaggtca	gtctagagca	cgaggagcag	aaactggagc	tcaagcgcca	gctcacagag	2760
ctacagctct	ccctgcagga	gcgcgagtca	cagttgacag	ccctgcaggc	tgcacgggcg	2820
gccctggaga	gccagcttcg	ccaggcgaag	acagagctgg	aagagaccac	agcagaagct	2880
gaagaggaga	tccaggcact	cacggcacat	agagatgaaa	tccagcgcaa	atttgatgct	2940
cttcgtaaca	gctgtactgt	aatcacagac	ctggaggagc	agctaaacca	gctgaccgag	3000
gacaacgctg	aactcaacaa	ccaaaacttc	tacttgtcca	aacaactcga	tgaggcttct	3060
ggcgccaacg	acgagattgt	acaactgcga	agtgaagtgg	accatctccg	ccgggagatc	3120
acggaacgag	agatgcagct	taccagccag	aagcaaacga	tggaggctct	gaagaccacg	3180
tgcaccatgc	tggaggaaca	ggtcatggat	ttggaggccc	taaacgatga	gctgctagaa	3240
aaagagcggc	agtgggaggc	ctggaggagc	gtcctgggtg	atgagaaatc	ccagtttgag	3300
tgtcgggttc	gagagctgca	gagaatgctg	gacaccgaga	aacagagcag	ggcgagagcc	3360
gatcagcggg	tcaccgagtc	tgcgccagtg	gtggagctgg	cagtgaagga	gcacaaggct	3420
gagattctcg	ctctgcagca	ggctctcaaa	gagcagaagc	tgaaggccga	gagcctctct	3480
gacaagctca	atgacctgga	gaagaagcat	gctatgcttg	aaatgaatgc	ccgaagctta	3540
cagcagaagc	tggagactga	acgagagctc	aaacagaggc	ttctggaaga	gcaagccaaa	3600
ttacagcagc	agatggacct	gcagaaaaat	cacattttcc	gtctgactca	aggactgcaa	3660
gaagctctag	atcgggctga	tctactgaag	acagaaaaga	gtgacttgga	gtatcagctg	3720
gaaaacattc	aggttctcta	ttctcatgaa	aagggtgaaa	tggaaaggcac	tattttctcaa	3780
caaaccaaaac	tcattgattt	tctgcaagcc	aaaatggacc	aacctgctaa	aaagaaaaag	3840
gttcctctgc	agtacaatga	gctgaagctg	gccctggaga	aggagaaaagc	tcgctgtgca	3900
gagctagagg	aagcccttca	gaagacccgc	atcgagctcc	ggtccgcccg	ggaggaagct	3960
gcccaccgca	aagcaacgga	ccaccacac	ccatccacgc	cagccaccgc	gaggcagcag	4020
atcgccatgt	ccgccatcgt	gcggtcgcca	gagcaccagc	ccagtgccat	gagcctgctg	4080
gccccgccat	ccagccgcag	aaaggagtct	tcaactccag	aggaatttag	tcggcgtctt	4140
aagggaacgca	tgcaccacaa	tattcctcac	cgattcaacg	taggactgaa	catgcgagcc	4200
acaaagtgtg	ctgtgtgtct	ggataaccgtg	cactttggac	gccaggcatc	caaattgtctc	4260
gaatgtcagg	tgatgtgtca	ccccaaagtgc	tccacgtgct	tgccagccac	ctgcggttg	4320
cctgctgaat	atgccacaca	cttcaccgag	gccttctgcc	gtgacaaaaat	gaactcccca	4380
ggtctccaga	ccaaggagcc	cagcagcagc	ttgcacctgg	aagggtggat	gaagggtgcc	4440
aggaataaca	aacgaggaca	gcaaggctgg	gacaggaagt	acattgtcct	ggaggggatca	4500
aaagtcctca	tttatgacaa	tgaagccaga	gaagtctggac	agaggccggt	ggaagaattt	4560

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Fig. 4 (continued)

gagctgtgcc	ttcccgacgg	ggatgtatct	attcatgggtg	ccgttggtgc	ttccgaactc	4620
gcaaatacag	ccaaagcaga	tgtcccatac	atactgaaga	tggaatctca	cccgcacacc	4680
acctgctggc	ccgggagaa	cctctacttg	ctagctccca	gcttccctga	caaacagcgc	4740
tgggtcaccg	ccttagaatc	agttgtcgca	ggtgggagag	tttctagggg	aaaagcagaa	4800
gctgatgcta	aactgcttgg	aaactccctg	ctgaaactgg	aagggtgatga	ccgtctagac	4860
atgaactgca	cgctgccctt	cagtgaccag	gtggtgttgg	tgggcaccga	ggaagggtctc	4920
tacgccctga	atgtcttgaa	aaactcccta	acccatgtcc	caggaattgg	agcagtcttc	4980
caaatttata	ttatcaagga	cctgggagaag	ctactcatga	tagcaggaga	agagcgggca	5040
ctgtgtcttg	tggacgtgaa	gaaagtgaaa	cagtccctgg	cccagtccca	cctgcctgcc	5100
cagcccgaca	tctcacccaa	cattttttgaa	gctgtcaagg	gctgccactt	gtttggggca	5160
ggcaagattg	agaacgggct	ctgcatctgt	gcagccatgc	ccagcaaagt	cgtcattctc	5220
cgctacaacg	aaaacctcag	caaatactgc	atccggaaaag	agatagagac	ctcagagccc	5280
tgcagctgta	tccacttcac	caattacagt	atcctcattg	gaaccaataa	attctacgaa	5340
atcgacatga	agcagtacac	gctcgaggaa	ttcctggata	agaatgacca	ttccttggca	5400
cctgctgtgt	ttgccgcctc	ttccaacagc	ttccctgtct	caatcgtgca	ggtgaacagc	5460
gcagggcagc	gagaggagta	cttgctgtgt	ttccacgaat	ttggagtgtt	cgtggattct	5520
tacggaagac	gtagccgcac	agacgatctc	aagtggagtc	gcttaccttt	ggcctttgcc	5580
tacagagaac	cctatctgtt	tgtgaccac	ttcaactcac	tcgaagtaat	tgagatccag	5640
gcacgctcct	cagcagggac	ccctgcccga	gcgtacctgg	acatcccga	cccgcgctac	5700
ctggggccctg	ccatttcctc	aggagcgatt	tacttggcgt	cctcatacca	ggataaatta	5760
agggtcattt	gctgcaaggg	aaacctcgtg	aaggagtccg	gcactgaaca	ccaccggggc	5820
ccgtccacct	ccgcagcag	ccccacaag	cgaggcccac	ccacgtacaa	cgagcacatc	5880
accaagcgcg	tggcctccag	cccagcgccg	cccgaaggcc	ccagccacc	gcgagagcca	5940
agcacacccc	accgctaccg	cgaggggagg	accgagctgc	gcagggacaa	gtctcctggc	6000
cgccccctgg	agcgagagaa	gtcccccgcc	cggatgctca	gcacgcggag	agagcgggtc	6060
cccgggaggc	tgtttgaaga	cagcagcagg	ggccggctgc	ctgcgggagc	cgtgaggacc	6120
ccgctgtccc	aggtgaacaa	ggtctgggac	cagtcttcag	tataaatctc	agccagaaaa	6180
accaactcct	catcttgatc	tgcaggaaaa	caccaaacc	actatggaac	tctgctgatg	6240
gggacccaag	cgcccacgtg	ctcagccacc	ctctggctca	gcggggccca	gacccacctc	6300
ggcacggaca	cccctgtctc	caggaggggc	aggtggctga	ggctcttcgg	agctgtcagc	6360
gcccggtgcc	tgcctggggc	acctccctgc	agtcactctc	ttgcactttg	ttactctttc	6420
aaagcattca	caaacttttg	tacctagctc	tagcctgtac	cagttagttc	atcaaaggaa	6480
accaaccggg	atgctaacaa	caacatgggt	agaatcctaa	ttagctactt	taagatccta	6540
ggattgggtg	gtttttcttt	ttttttcttc	tttggttctt	tccttttttt	tttttttttt	6600
taagacaaca	gaattcttaa	tagatttgaa	tagcgacgta	tttcctgttg	tagtcatttt	6660
tagctcgacc	acatcatcag	gtctttgcca	ccgaggcata	gtgtagaaca	gtcccgggtc	6720
gttggccaac	ctccgcagc	caagtaggtt	catccttggt	cctgttcatt	ctcatagatg	6780

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Fig. 4 (continued)

gccctgcttt	ccccaggggtg	acatcgtagc	caaatgttta	ctgttttcat	tgccttttat	6840
ggccttgacg	acttcccctc	ccaccagctg	agaatgtatg	gaggtcatcg	gggcctcagc	6900
tcggaggcag	tgacttgggg	ccaagggacc	tcgagacgct	ttccttcccc	accccccagc	6960
gtcatctccc	cagcctgctg	ttcccgcctt	ccatatagct	ttggccagga	aagcatgcaa	7020
tagacttgct	cggagcccag	cactcctggg	tctcggggtc	ggggagggga	cgggggcacc	7080
cacttccttg	tctgtgacgg	cgtgttggtc	cccactctgg	gatggggaag	aggcccgcgc	7140
ggagtctctg	atggcagttc	actgcatgtg	ctgccccctt	gggttgctct	gccaatgtat	7200
taataccatc	ccatagctcc	tgccaaatcg	agaccctctg	acgacttgcc	gactaactgg	7260
ccaccacaag	ctgcagtctg	tagcactgaa	caaacaaaaa	acaaaacgct	caagccttac	7320
gaccagagaa	ggatttcagc	aaaccaccac	ctcccactca	gtgtcccctc	caaacttcac	7380
acttccctgc	ctgcagagga	tgactctggt	cacacccaat	ccagcgcggt	tctaccccac	7440
gaaactgtga	ctttccaaat	gagcctttcc	ctaggggctag	acctaagacc	aggaagtgtg	7500
agaaagcagc	cgcagctcaa	ctcttccagc	tccgccaggg	ttgggaagtc	cttaggtgca	7560
gtgcggtccc	cactgggtct	gcggaccctc	ctattagagt	acgaaattcc	tggcaactgg	7620
tatagaacca	acctagaggc	tttgagttg	gcaagctaac	tcgcggcctt	atttctgcct	7680
ttaatctccc	acaaggcatc	tgttgctttg	ggtcctccac	gactcttagg	ccgcctcaa	7740
caaccaggc	acctcctagg	taggctcaaa	ggtagaccgc	ttccaccgc	agcaggtgaa	7800
catgaccgtg	ttttcaactg	tgtccacagt	tcagatccct	ttccagattg	caacctggcc	7860
tgcaccccag	ctccttccctg	ctcgtgtctt	aacctaaagt	ctttcttggt	tgaaacgcct	7920
acaaacctcc	atgtggtagc	tcctttggca	aatgtcctgc	tgtggcgttt	tatgtgttgc	7980
ttggagtctg	tggggtcgta	ctccctcccc	tcccgctccc	agggcagatt	tgattgaatg	8040
tttgctgaag	ttttgtctct	tgggtccacag	tatttggaag	ggtcactgaa	aatgggtcct	8100
tcagtcttgg	catttcattt	aggatctcca	tgagaaatgg	gcttcttgag	ccctgaaaat	8160
gtatatattg	tgtctcatct	gtgaactgct	ttctgctata	tagaactagc	tcaaaagact	8220
gtacatattt	acaagaaact	ttatatctgt	aaaaaaaaaa	agaggaaatt	gaattggttt	8280
ctactttttt	attgtaaaag	gtgcattttt	caacacttac	ttttggtttc	aatgggtggt	8340
gttgtggaca	gccatcttca	ctggaggggtg	gggagctccg	tgtgaccacc	aagatgccag	8400
caggatatac	cgtaacacga	aattgctgtc	aaaagcttat	tagcatcaat	caagattcta	8460
ggtctccaaa	agtacaggct	ttttcttcat	tacctttttt	attcagaacg	aggaagagaa	8520
cacaaggaat	gattcaagat	ccaccttgag	aggaatgaac	tttggtgttg	aacaattagt	8580
gaaataaagc	aatgatctaa	act				8603

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Fig. 5

Val	Leu	Asp	Asn	Gln	Ile	Lys	Lys	Asp	Leu	Ala	Asp	Lys	Glu	Thr	Leu
1				5					10					15	
Glu	Asn	Met	Met	Gln	Arg	His	Glu	Glu	Glu	Ala	His	Glu	Lys	Gly	Lys
			20					25					30		
Ile	Leu	Ser	Glu	Gln	Lys	Ala	Met	Ile	Asn	Ala	Met	Asp	Ser	Lys	Ile
		35					40					45			
Arg	Ser	Leu	Glu	Gln	Arg	Ile	Val	Glu	Leu	Ser	Glu	Ala	Asn	Lys	Leu
		50				55					60				
Ala	Ala	Asn	Ser	Ser	Leu	Phe	Thr	Gln	Arg	Asn	Met	Lys	Ala	Gln	Glu
65					70				75					80	
Glu	Met	Ile	Ser	Glu	Leu	Arg	Gln	Gln	Lys	Phe	Tyr	Leu	Glu	Thr	Gln
				85					90					95	
Ala	Gly	Lys	Leu	Glu	Ala	Gln	Asn	Arg	Lys	Leu	Glu	Glu	Gln	Leu	Glu
			100					105					110		
Lys	Ile	Ser	His	Gln	Asp	His	Ser	Asp	Lys	Asn	Arg	Leu	Leu	Glu	Leu
		115					120					125			
Glu	Thr	Arg	Leu	Arg	Glu	Val	Ser	Leu	Glu	His	Glu	Glu	Gln	Lys	Leu
		130				135					140				
Glu	Leu	Lys	Arg	Gln	Leu	Thr	Glu	Leu	Gln	Leu	Ser	Leu	Gln	Glu	Arg
145					150				155					160	
Glu	Ser	Gln	Leu	Thr	Ala	Leu	Gln	Ala	Ala	Arg	Ala	Ala	Leu	Glu	Ser
				165				170					175		
Gln	Leu	Arg	Gln	Ala	Lys	Thr	Glu	Leu	Glu	Glu	Thr	Thr	Ala	Glu	Ala
		180						185					190		
Glu	Glu	Glu	Ile	Gln	Ala	Leu	Thr	Ala	His	Arg	Asp	Glu	Ile	Gln	Arg
		195					200				205				
Lys	Phe	Asp	Ala	Leu	Arg	Asn	Ser	Cys	Thr	Val	Ile	Thr	Asp	Leu	Glu
	210					215					220				
Glu	Gln	Leu	Asn	Gln	Leu	Thr	Glu	Asp	Asn	Ala	Glu	Leu	Asn	Asn	Gln
225				230					235					240	
Asn	Phe	Tyr	Leu	Ser	Lys	Gln	Leu	Asp	Glu	Ala	Ser	Gly	Ala	Asn	Asp
				245					250				255		
Glu	Ile	Val	Gln	Leu	Arg	Ser	Glu	Val	Asp	His	Leu	Arg	Arg	Glu	Ile
		260						265				270			
Thr	Glu	Arg	Glu	Met	Gln	Leu	Thr	Ser	Gln	Lys	Gln	Thr	Met	Glu	Ala
		275					280					285			
Leu	Lys	Thr	Thr	Cys	Thr	Met	Leu	Glu	Glu	Gln	Val	Met	Asp	Leu	Glu
	290					295					300				

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Fig. 5 (continued)

Ala	Leu	Asn	Asp	Glu	Leu	Leu	Glu	Lys	Glu	Arg	Gln	Trp	Glu	Ala	Trp
305					310					315					320
Arg	Ser	Val	Leu	Gly	Asp	Glu	Lys	Ser	Gln	Phe	Glu	Cys	Arg	Val	Arg
				325					330					335	
Glu	Leu	Gln	Arg	Met	Leu	Asp	Thr	Glu	Lys	Gln	Ser	Arg	Ala	Arg	Ala
				340					345					350	
Asp	Gln	Arg	Ile	Thr	Glu	Ser	Arg	Gln	Val	Val	Glu	Leu	Ala	Val	Lys
				355				360					365		
Glu	His	Lys	Ala	Glu	Ile	Leu	Ala	Leu	Gln	Gln	Ala	Leu	Lys	Glu	Gln
				370				375				380			
Lys	Leu	Lys	Ala	Glu	Ser	Leu	Ser	Asp	Lys	Leu	Asn	Asp	Leu	Glu	Lys
385						390					395				400
Lys	His	Ala	Met	Leu	Glu	Met	Asn	Ala	Arg	Ser	Leu	Gln	Gln	Lys	Leu
				405					410					415	
Glu	Thr	Glu	Arg	Glu	Leu	Lys	Gln	Arg	Leu	Leu	Glu	Glu	Gln	Ala	Lys
				420					425					430	
Leu	Gln	Gln	Gln	Met	Asp	Leu	Gln	Lys	Asn	His	Ile	Phe	Arg	Leu	Thr
				435					440				445		
Gln	Gly	Leu	Gln	Glu	Ala	Leu	Asp	Arg	Ala	Asp	Leu	Leu	Lys	Thr	Glu
				450					455				460		
Arg	Ser	Asp	Leu	Glu	Tyr	Gln	Leu	Glu	Asn	Ile	Gln	Val	Leu	Tyr	Ser
465						470					475				480
His	Glu	Lys	Val	Lys	Met	Glu	Gly	Thr	Ile	Ser	Gln	Gln	Thr	Lys	Leu
				485					490					495	
Ile	Asp	Phe	Leu	Gln	Ala	Lys	Met	Asp	Gln	Pro	Ala	Lys	Lys	Lys	Lys
				500					505				510		
Val	Pro	Leu	Gln	Tyr	Asn	Glu	Leu	Lys	Leu	Ala	Leu	Glu	Lys	Glu	Lys
				515					520				525		
Ala	Arg	Cys	Ala	Glu	Leu	Glu	Glu	Ala	Leu	Gln	Lys	Thr	Arg	Ile	Glu
				530				535				540			
Leu	Arg	Ser	Ala	Arg	Glu	Glu	Ala	Ala	His	Arg	Lys	Ala	Thr	Asp	His
545						550				555					560
Pro	His	Pro	Ser	Thr	Pro	Ala	Thr	Ala	Arg	Gln	Gln	Ile	Ala	Met	Ser
				565					570					575	
Ala	Ile	Val	Arg	Ser	Pro	Glu	His	Gln	Pro	Ser	Ala	Met	Ser	Leu	Leu
				580					585				590		
Ala	Pro	Pro	Ser	Ser	Arg	Arg	Lys	Glu	Ser	Ser	Thr	Pro	Glu	Glu	Phe
				595				600					605		

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Fig. 5 (continued)

Ser	Arg	Arg	Leu	Lys	Glu	Arg	Met	His	His	Asn	Ile	Pro	His	Arg	Phe
610						615					620				
Asn	Val	Gly	Leu	Asn	Met	Arg	Ala	Thr	Lys	Cys	Ala	Val	Cys	Leu	Asp
625				630						635				640	
Thr	Val	His	Phe	Gly	Arg	Gln	Ala	Ser	Lys	Cys	Leu	Glu	Cys	Gln	Val
				645					650					655	
Met	Cys	His	Pro	Lys	Cys	Ser	Thr	Cys	Leu	Pro	Ala	Thr	Cys	Gly	Leu
			660					665					670		
Pro	Ala	Glu	Tyr	Ala	Thr	His	Phe	Thr	Glu	Ala	Phe	Cys	Arg	Asp	Lys
	675						680					685			
Met	Asn	Ser	Pro	Gly	Leu	Gln	Thr	Lys	Glu	Pro	Ser	Ser	Ser	Leu	His
690						695					700				
Leu	Glu	Gly	Trp	Met	Lys	Val	Pro	Arg	Asn	Asn	Lys	Arg	Gly	Gln	Gln
705					710					715				720	
Gly	Trp	Asp	Arg	Lys	Tyr	Ile	Val	Leu	Glu	Gly	Ser	Lys	Val	Leu	Ile
				725					730					735	
Tyr	Asp	Asn	Glu	Ala	Arg	Glu	Ala	Gly	Gln	Arg	Pro	Val	Glu	Glu	Phe
			740					745					750		
Glu	Leu	Cys	Leu	Pro	Asp	Gly	Asp	Val	Ser	Ile	His	Gly	Ala	Val	Gly
	755						760					765			
Ala	Ser	Glu	Leu	Ala	Asn	Thr	Ala	Lys	Ala	Asp	Val	Pro	Tyr	Ile	Leu
770						775					780				
Lys	Met	Glu	Ser	His	Pro	His	Thr	Thr	Cys	Trp	Pro	Gly	Arg	Thr	Leu
785					790					795				800	
Tyr	Leu	Leu	Ala	Pro	Ser	Phe	Pro	Asp	Lys	Gln	Arg	Trp	Val	Thr	Ala
				805					810					815	
Leu	Glu	Ser	Val	Val	Ala	Gly	Gly	Arg	Val	Ser	Arg	Glu	Lys	Ala	Glu
			820					825					830		
Ala	Asp	Ala	Lys	Leu	Leu	Gly	Asn	Ser	Leu	Leu	Lys	Leu	Glu	Gly	Asp
	835						840				845				
Asp	Arg	Leu	Asp	Met	Asn	Cys	Thr	Leu	Pro	Phe	Ser	Asp	Gln	Val	Val
850					855						860				
Leu	Val	Gly	Thr	Glu	Glu	Gly	Leu	Tyr	Ala	Leu	Asn	Val	Leu	Lys	Asn
865					870				875					880	
Ser	Leu	Thr	His	Val	Pro	Gly	Ile	Gly	Ala	Val	Phe	Gln	Ile	Tyr	Ile
				885					890					895	
Ile	Lys	Asp	Leu	Glu	Lys	Leu	Leu	Met	Ile	Ala	Gly	Glu	Glu	Arg	Ala
			900					905					910		

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Fig. 5 (continued)

Leu Cys Leu Val Asp Val Lys Lys Val Lys Gln Ser Leu Ala Gln Ser		
915	920	925
His Leu Pro Ala Gln Pro Asp Ile Ser Pro Asn Ile Phe Glu Ala Val		
930	935	940
Lys Gly Cys His Leu Phe Gly Ala Gly Lys Ile Glu Asn Gly Leu Cys		
945	950	955
Ile Cys Ala Ala Met Pro Ser Lys Val Val Ile Leu Arg Tyr Asn Glu		
965	970	975
Asn Leu Ser Lys Tyr Cys Ile Arg Lys Glu Ile Glu Thr Ser Glu Pro		
980	985	990
Cys Ser Cys Ile His Phe Thr Asn Tyr Ser Ile Leu Ile Gly Thr Asn		
995	1000	1005
Lys Phe Tyr Glu Ile Asp Met Lys Gln Tyr Thr Leu Glu Glu Phe Leu		
1010	1015	1020
Asp Lys Asn Asp His Ser Leu Ala Pro Ala Val Phe Ala Ala Ser Ser		
1025	1030	1035
Asn Ser Phe Pro Val Ser Ile Val Gln Val Asn Ser Ala Gly Gln Arg		
1045	1050	1055
Glu Glu Tyr Leu Leu Cys Phe His Glu Phe Gly Val Phe Val Asp Ser		
1060	1065	1070
Tyr Gly Arg Arg Ser Arg Thr Asp Asp Leu Lys Trp Ser Arg Leu Pro		
1075	1080	1085
Leu Ala Phe Ala Tyr Arg Glu Pro Tyr Leu Phe Val Thr His Phe Asn		
1090	1095	1100
Ser Leu Glu Val Ile Glu Ile Gln Ala Arg Ser Ser Ala Gly Thr Pro		
1105	1110	1115
Ala Arg Ala Tyr Leu Asp Ile Pro Asn Pro Arg Tyr Leu Gly Pro Ala		
1125	1130	1135
Ile Ser Ser Gly Ala Ile Tyr Leu Ala Ser Ser Tyr Gln Asp Lys Leu		
1140	1145	1150
Arg Val Ile Cys Cys Lys Gly Asn Leu Val Lys Glu Ser Gly Thr Glu		
1155	1160	1165
His His Arg Gly Pro Ser Thr Ser Arg Ser Ser Pro Asn Lys Arg Gly		
1170	1175	1180
Pro Pro Thr Tyr Asn Glu His Ile Thr Lys Arg Val Ala Ser Ser Pro		
1185	1190	1195
Ala Pro Pro Glu Gly Pro Ser His Pro Arg Glu Pro Ser Thr Pro His		
1205	1210	1215

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Fig. 5 (continued)

Arg Tyr Arg Glu Gly Arg Thr Glu Leu Arg Arg Asp Lys Ser Pro Gly
1220 1225 1230
Arg Pro Leu Glu Arg Glu Lys Ser Pro Gly Arg Met Leu Ser Thr Arg
1235 1240 1245
Arg Glu Arg Ser Pro Gly Arg Leu Phe Glu Asp Ser Ser Arg Gly Arg
1250 1255 1260
Leu Pro Ala Gly Ala Val Arg Thr Pro Leu Ser Gln Val Asn Lys Val
1265 1270 1275 1280
Trp Asp Gln Ser Ser Val
1285

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Fig. 6

cagagcaggg	cgagagccga	tcagcggatc	accgagtctc	gccaggtggt	ggagctggca	60
gtgaaggagc	acaaggctga	gattctcgct	ctgcagcagg	ctctcaaaga	gcagaagctg	120
aaggccgaga	gcctctctga	caagctcaat	gacctggaga	agaagcatgc	tatgcttgaa	180
atgaatgccc	gaagcttaca	gcagaagctg	gagactgaac	gagagctcaa	acagaggctt	240
ctggaagagc	aagccaaatt	acagcagcag	atggacctgc	agaaaaatca	cattttccgt	300
ctgactcaag	gactgcaaga	agctctagat	cgggctgata	tactgaagac	agaaagaagt	360
gacttgaggt	atcagctgga	aaacattcag	gttctctatt	ctcatgaaaa	ggtgaaaatg	420
gaaggcacta	tttctcaaca	aaccaaactc	attgattttc	tgcaagccaa	aatggacca	480
cctgctaaaa	agaaaaaggt	tcctctgcag	tacaatgagc	tgaagctggc	cctggagaag	540
gagaaagctc	gctgtgcaga	gctagaggaa	gcccttcaga	agaccgcgat	cgagctccgg	600
tccgcccggg	aggaagctgc	ccaccgcaaa	gcaacggacc	accacacccc	atccacgcca	660
gccaccgcga	ggcagcagat	cgccatgtct	gccatcgtgc	ggtcgccaga	gcaccagccc	720
agtgccatga	gcctgctggc	cccgccatcc	agccgcagaa	aggagtcttc	aactccagag	780
gaatttagtc	ggcgtcttaa	ggaacgcgat	caccacaata	ttcctcaccg	attcaacgta	840
ggactgaaca	tgcgagccac	aaagtgtgct	gtgtgtctgg	ataccgtgca	ctttggacgc	900
caggcatcca	aatgtctcga	atgtcaggtg	atgtgtcacc	ccaagtgctc	cacgtgcttg	960
ccagccacct	gcggcttgcc	tgtgaatat	gccacacact	tcaccgaggc	cttctgcctg	1020
gacaaaatga	actccccagg	tctccagacc	aaggagccca	gcagcagctt	gcacctggaa	1080
gggtggatga	aggtgcccag	gaataacaaa	cgaggacagc	aaggctggga	caggaagtac	1140
attgtcctgg	agggatcaaa	agtccctcatt	tatgacaatg	aagccagaga	agctggacag	1200
aggccggtgg	agaattttga	gctgtgcctt	cccgcggggg	atgtatctat	tcatggtgcc	1260
gttggtgctt	ccgaactcgc	aaatacagcc	aaagcagatg	tccatacat	actgaagatg	1320
gaatctcacc	cgcacaccac	ctgctggccc	gggagaaccc	tctacttgct	agctcccagc	1380
ttccctgaca	aacagcgcgt	ggtcaccgcc	ttagaatcag	ttgtcgcagg	tgggagagtt	1440
tctagggaaa	aagcagaagc	tgatgctaaa	ctgcttgga	actccctgct	gaaactggaa	1500
gggtgatgacc	gtctagacat	gaactgcacg	ctgcccttca	gtgaccaggt	ggtgttggtg	1560
ggcaccgagg	aagggtctta	cgccctgaat	gtcttgaaaa	actccctaac	ccatgtccca	1620
ggaattggag	cagtcttcca	aatttatatt	atcaaggacc	tggagaagct	actcatgata	1680
gcaggagaag	agcgggcact	gtgtcttggt	gacgtgaaga	aagtgaaaca	gtccctggcc	1740
cagtcccacc	tgcttgccca	gcccgcacatc	tcacccaaca	tttttgaaagc	tgtcaagggc	1800
tgccacttgt	ttggggcagg	caagattgag	aacgggctct	gcactctgtgc	agccatgccc	1860
agcaaagtcg	tcattctccg	ctacaacgaa	aacctcagca	aatactgcat	ccggaaagag	1920
atagagacct	cagagccctg	cagctgtatc	cacttcacca	attacagtat	cctcattgga	1980
accaataaat	tctacgaaat	cgacatgaag	cagtacacgc	tcgaggaatt	cctggataag	2040
aatgaccatt	ccttggcacc	tgtgtgtgtt	gccgcctctt	ccaacagctt	ccctgtctca	2100
atcgtgcagg	tgaacagcgc	agggcagcga	gaggagtact	tgctgtgttt	ccacgaattt	2160
ggagtgttcg	tggattctta	cggaagacgt	agccgcacag	acgatctcaa	gtggagtgcg	2220
ttacctttgg	cctttgccta	cagagaaccc	tatctgtttg	tgaccactt	caactcactc	2280

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Fig. 6 (continued)

gaagtaattg	agatccaggc	acgctcctca	gcagggaccc	ctgcccagagc	gtacctggac	2340
atcccgaacc	cgcgctacct	gggccctgcc	atttcctcag	gagcgattta	cttggcgctcc	2400
tcataccagg	ataaattaag	ggtcatttgc	tgcaagggaa	acctcgtgaa	ggagtccggc	2460
actgaacacc	accggggccc	gtccacctcc	cgcagcagcc	ccaacaagcg	aggcccaccc	2520
acgtacaacg	agcacatcac	caagcgcgtg	gcctccagcc	cagcgccgoc	cgaaggcccc	2580
agccaccgcg	gagagccaag	cacaccccac	cgctaccgcg	aggggcggac	cgagctgcgc	2640
agggacaagt	ctcctggccg	ccccctggag	cgagagaagt	ccccggccg	gatgctcagc	2700
acgcggagag	agcgggtccc	cgggaggctg	tttgaagaca	gcagcagggg	ccggctgcct	2760
gcgggagccg	tgaggacccc	gctgtcccag	gtgaacaagg	tctgggacca	gtcttcagta	2820
taaatctcag	ccagaaaaac	caactcctca	tcttgatctg	caggaaaaca	ccaaacacac	2880
tatggaactc	tgctgatggg	gacccaagcg	cccacgtgct	cagccaccct	ctggctcagc	2940
ggggcccaga	cccacctcgg	cacggacacc	cctgtctcca	ggaggggcag	gtggctgagg	3000
ctcttcggag	ctgtcagcgc	ccggtgcctg	ccctgggcac	ctccctgcag	tcctctcttt	3060
gcactttgtt	actctttcaa	agcattcaca	aacttttgta	cctagctcta	gcctgtacca	3120
gttagttcat	caaaggaaac	caaccgggat	gctaacaaca	acatggttag	aatcctaatt	3180
agctacttta	agatcctagg	attgggttgt	ttttcttttt	ttttctctct	tgtttctttc	3240
cttttttttt	ttttttttta	agacaacaga	attcttaata	gatttgaata	gcgacgtatt	3300
tcctgttgta	gtcattttta	gctcgaccac	atcatcaggt	ctttgccacc	gaggcatagt	3360
gtagaacagt	cccggtcagt	tggccaacct	cccgcagcca	agtaggttca	tccttggtcc	3420
tgttcattct	catagatggc	cctgctttcc	ccagggtgac	atcgtagcca	aatgtttact	3480
gttttcattg	ccttttatgg	ccttgacgac	ttcccctccc	accagctgag	aatgtatgga	3540
ggtcatcggg	gcctcagctc	ggaggcagtg	acttggggcc	aagggaacct	gagacgcttt	3600
ccttccccac	ccccagcgt	catctcccca	gcctgctgtt	cccgttttcc	atatagcttt	3660
ggccaggaaa	gcatgcaata	gacttgctcg	gagcccagca	ctcctgggtc	tcggggtcgg	3720
ggaggggacg	ggggcaccca	cttccttgtc	tgtgacggcg	tggtgttccc	cactctggga	3780
tggggaagag	gcccgtcggg	agttctgcat	ggcagttcac	tgcagtgtgt	gcccccttgg	3840
gttgctctgc	caatgtatta	ataccatccc	atagctcctg	ccaaatcgag	accctctgac	3900
gacttgccga	ctaactggcc	accacaagct	gcagtctgta	gcactgaaca	aacaaaaaac	3960
aaaacgctca	agccttacga	ccagagaagg	atttcagcaa	accaccacct	cccactcagt	4020
gtcccctcca	aacttcacac	ttccctgcct	gcagaggatg	actctgttca	cacccaatcc	4080
agcgcgggtc	tacccacga	aactgtgact	ttccaaatga	gcctttccct	agggctagac	4140
ctaagaccag	gaagtttgag	aaagcagccg	cagctcaact	cttcagctc	cgccagggtt	4200
gggaagtcct	taggtgcagt	gcggctccca	ctgggtctgc	ggaccctcct	attagagtac	4260
gaaattcctg	gcaactggta	tagaaccaac	ctagaggctt	tgcagttggc	aagctaactc	4320
gcggccctat	ttctgccttt	aatctcccac	aaggcatctg	ttgctttggg	tcctccacga	4380
ctcttaggcc	cgcctcaaca	accaggcac	ctcctaggta	ggctcaaagg	tagaccogtt	4440
tccaccgcag	caggtgaaca	tgaccgtgtt	ttcaactgtg	tccacagttc	agatcccttt	4500
ccagattgca	acctggcctg	catcccagct	ccttcctgct	cgtgtcttaa	cctaagtgtc	4560
ttcttggttg	aaacgcctac	aaacctccat	gtggtagctc	ctttggcaaa	tgtcctgctg	4620

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Fig. 6 (continued)

tggcgtttta	tgtgttgctt	ggagtctgtg	gggtcgtact	ccctcccctc	ccgtccccag	4680
ggcagatttg	attgaatggt	tgttgaagtt	ttgtctcttg	gtccacagta	tttggaagg	4740
tcactgaaaa	tgggtctttc	agtcttggca	tttcatttag	gatctccatg	agaaatgggc	4800
ttcttgagcc	ctgaaaatgt	atattgtgtg	tctcatctgt	gaactgcttt	ctgctatata	4860
gaactagctc	aaaagactgt	acataattac	aagaaacttt	atattcgtaa	aaaaaaaaag	4920
aggaaattga	attgggtttct	acttttttat	tgtaaaaggt	gcatttttca	acacttactt	4980
ttggtttcaa	tggtggtagt	tgtggacagc	catcttcact	ggagggtggg	gagctccgtg	5040
tgaccaccaa	gatgccagca	ggatataccg	taacacgaaa	ttgctgtcaa	aagcttatta	5100
gcatcaatca	agattctagg	tctccaaaag	tacaggcttt	ttcttcatta	ccttttttat	5160
tcagaacgag	gaagagaaca	caaggaatga	ttcaagatcc	accttgagag	gaatgaactt	5220
tgttggtgaa	caattagtga	aataaagcaa	tgatctaaac	t		5261

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Fig. 7

Met	Ser	Ala	Glu	Val	Arg	Leu	Arg	Gln	Leu	Gln	Gln	Leu	Val	Leu	Asp	1	5	10	15
Pro	Gly	Phe	Leu	Gly	Leu	Glu	Pro	Leu	Leu	Asp	Leu	Leu	Leu	Gly	Val	20	25	30	
His	Gln	Glu	Leu	Gly	Ala	Ser	His	Leu	Ala	Gln	Asp	Lys	Tyr	Val	Ala	35	40	45	
Asp	Phe	Leu	Gln	Trp	Val	Glu	Pro	Ile	Ala	Ala	Arg	Leu	Lys	Glu	Val	50	55	60	
Arg	Leu	Gln	Arg	Asp	Asp	Phe	Glu	Ile	Leu	Lys	Val	Ile	Gly	Arg	Gly	65	70	75	80
Ala	Phe	Ser	Glu	Val	Ala	Val	Val	Lys	Met	Lys	Gln	Thr	Gly	Gln	Val	85	90	95	
Tyr	Ala	Met	Lys	Ile	Met	Asn	Lys	Trp	Asp	Met	Leu	Lys	Arg	Gly	Glu	100	105	110	
Val	Ser	Cys	Phe	Arg	Glu	Glu	Arg	Asp	Val	Leu	Val	Lys	Gly	Asp	Arg	115	120	125	
Arg	Trp	Ile	Thr	Gln	Leu	His	Phe	Ala	Phe	Gln	Asp	Glu	Asn	Tyr	Leu	130	135	140	
Tyr	Leu	Val	Met	Glu	Tyr	Tyr	Val	Gly	Gly	Asp	Leu	Leu	Thr	Leu	Leu	145	150	155	160
Ser	Lys	Phe	Gly	Glu	Arg	Ile	Pro	Ala	Glu	Met	Ala	Arg	Phe	Tyr	Leu	165	170	175	
Ala	Glu	Ile	Val	Met	Ala	Ile	Asp	Ser	Val	His	Arg	Leu	Gly	Tyr	Val	180	185	190	
His	Arg	Asp	Ile	Lys	Pro	Asp	Asn	Ile	Leu	Leu	Asp	Arg	Cys	Gly	His	195	200	205	
Ile	Arg	Leu	Ala	Asp	Phe	Gly	Ser	Cys	Leu	Lys	Leu	Gln	Pro	Asp	Gly	210	215	220	
Met	Val	Arg	Ser	Leu	Val	Ala	Val	Gly	Thr	Pro	Asp	Tyr	Leu	Ser	Pro	225	230	235	240
Glu	Ile	Leu	Gln	Ala	Val	Gly	Gly	Gly	Pro	Gly	Ala	Gly	Ser	Tyr	Gly	245	250	255	
Pro	Glu	Cys	Asp	Trp	Trp	Ala	Leu	Gly	Val	Phe	Ala	Tyr	Glu	Met	Phe	260	265	270	
Tyr	Gly	Gln	Thr	Pro	Phe	Tyr	Ala	Asp	Ser	Thr	Ala	Glu	Thr	Tyr	Ala	275	280	285	

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Fig. 7 (continued)

Lys	Ile	Val	His	Tyr	Arg	Glu	His	Leu	Ser	Leu	Pro	Leu	Ala	Asp	Thr
290						295					300				
Val	Val	Pro	Glu	Glu	Ala	Gln	Asp	Leu	Ile	Arg	Gly	Leu	Leu	Cys	Pro
305					310					315					320
Ala	Glu	Ile	Arg	Leu	Gly	Arg	Gly	Gly	Ala	Gly	Asp	Phe	Gln	Lys	His
				325					330					335	
Pro	Phe	Phe	Phe	Gly	Leu	Asp	Trp	Glu	Gly	Leu	Arg	Asp	Ser	Val	Pro
				340				345					350		
Pro	Phe	Thr	Pro	Asp	Phe	Glu	Gly	Ala	Thr	Asp	Thr	Cys	Asn	Phe	Asp
		355					360					365			
Val	Val	Glu	Asp	Arg	Leu	Thr	Ala	Met	Val	Ser	Gly	Gly	Gly	Glu	Thr
		370				375					380				
Leu	Ser	Asp	Met	Gln	Glu	Asp	Met	Pro	Leu	Gly	Val	Arg	Leu	Pro	Phe
385				390						395					400
Val	Gly	Tyr	Ser	Tyr	Cys	Cys	Met	Ala	Phe	Arg	Asp	Asn	Gln	Val	Pro
				405					410					415	
Asp	Pro	Thr	Pro	Met	Glu	Leu	Glu	Ala	Leu	Gln	Leu	Pro	Val	Ser	Asp
			420					425					430		
Leu	Gln	Gly	Leu	Asp	Leu	Gln	Pro	Pro	Val	Ser	Pro	Pro	Asp	Gln	Val
		435					440						445		
Ala	Glu	Glu	Ala	Asp	Leu	Val	Ala	Val	Pro	Ala	Pro	Val	Ala	Glu	Ala
		450				455					460				
Glu	Thr	Thr	Val	Thr	Leu	Gln	Gln	Leu	Gln	Glu	Ala	Leu	Glu	Glu	Glu
465					470					475					480
Val	Leu	Thr	Arg	Gln	Ser	Leu	Ser	Arg	Glu	Leu	Glu	Ala	Ile	Arg	Thr
				485					490					495	
Ala	Asn	Gln	Asn	Phe	Ser	Ser	Gln	Leu	Gln	Glu	Ala	Glu	Val	Arg	Asn
			500					505					510		
Arg	Asp	Leu	Glu	Ala	His	Val	Arg	Gln	Leu	Gln	Glu	Arg	Met	Glu	Met
		515					520					525			
Leu	Gln	Ala	Pro	Gly	Ala	Ala	Ala	Ile	Thr	Gly	Val	Pro	Ser	Pro	Arg
		530				535					540				
Ala	Thr	Asp	Pro	Pro	Ser	His	Leu	Asp	Gly	Pro	Pro	Ala	Val	Ala	Val
545					550					555					560
Gly	Gln	Cys	Pro	Leu	Val	Gly	Pro	Gly	Pro	Met	His	Arg	Arg	His	Leu
				565					570					575	
Leu	Leu	Pro	Ala	Arg	Ile	Pro	Arg	Pro	Gly	Leu	Ser	Glu	Ala	Arg	Cys
			580				585						590		

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Fig. 7 (continued)

Leu	Leu	Leu	Phe	Ala	Ala	Ala	Leu	Ala	Ala	Ala	Ala	Thr	Leu	Gly	Cys
595						600						605			
Thr	Gly	Leu	Val	Ala	Tyr	Thr	Gly	Gly	Leu	Thr	Pro	Val	Trp	Cys	Phe
610						615						620			
Pro	Gly	Ala	Thr	Phe	Ala	Pro									
625						630									

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Fig. 8

BLASTP - alignment of 543_Protein against trembl|AF086824|AF086824_1
 gene: "Crik"; product: "rho/rac-interacting citron kinase"; Mus musculus
 rho/rac-interacting citron kinase (Crik) mRNA, complete cds.
 //:gp|AF086824|3599509 gene: "Crik"; product: "rho/rac-interacting citron
 kinase"; Mus musculus rho/rac-interacting citron kinase (Crik) mRNA,
 complete cds.

This hit is scoring at : 0.0 (expectation value)

Alignment length (overlap) : 2056

Identities : 96 %

Scoring matrix : BLOSUM62 (used to infer consensus pattern)

Database searched : nrdb_1_;

Q: 1 MLKFKYGARNPLDAGAAEPIASRASRLNLFFQGKPPFMTQQQMSPLSREGILDALFVLFE
 MLKFKYG.RNP :A.A:EPIASRASRLNLFFQGKPP.MTQQQMS.LSREG:LDALF.LFE
 H: 1 MLKFKYGVNPPPEASASEPIASRASRLNLFFQGKPLMTQQQMSALSREGMLDALFALFE

Protein_Kinase_ATP Motif (K binds ATP)

ECSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCGHFAEVQVVREKATG
 ECSQPALMK:KHVS:FV:KYSDTIAEL:ELQPSA:DFEVRSLVGCGHFAEVQVVREKATG
 ECSQPALMKMKHVSSFVQKYSDTIAELRELQPSARDFEVRSLVGCGHFAEVQVVREKATG

DIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLYLVMEYQPGG
 D:YAMK:MKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKN:LYLVMEYQPGG
 DVYAMKIMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNNLYLVMEYQPGG

Protein_Kinase_ST Motif (D is an active site)

DLLSLLNRYEDQLDENLIQFYLAELILAVHSVHLMGYVHRDIKPENILVDRTGHIKLVDF
 D.LSLLNRYEDQLDE: :IQFYLAELILAVHSVH MGYVHRDIKPENIL:DRTG.IKLVDF
 DFLSLLNRYEDQLDESMIQFYLAELILAVHSVHQMGYVHRDIKPENILIDRTGEIKLVDF

GSAAKMNSNKMVNAKLPIGTPDYMAPEVLTVMNGDGKGTYGLDCDWWSVGVIAYEMIYGR
 GSAAKMNSNK V:AKLPIGTPDYMAPEVLTVMN D :GTYGLDCDWWSVG:AYEM:YG:
 GSAAKMNSNK-VD AKLPIGTPDYMAPEVLTVMNEDRRGTYGLDCDWWSVG VVAYEMVY GK

SPFAEGTSARTFNNIMNFQRFKFPDDPKVSSDFLDLIQSLLCGQKERLKFEGLCCHPFF
 :PF.EGTSARTFNNIMNFQRFKFPDDPKVSS:.LDL:QSLLC QKERLKFEGLCCHPFF
 TPFTEGTSARTFNNIMNFQRFKFPDDPKVSSSELLDLLQSLLCVQKERLKFEGLCCHPFF

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Fig. 8 (continued)

SKIDWNNIRNSPPPFVPTLKSDDDTSNFDEPEKNSWSSSPCQLSPSGFSGEELPFVGFSS
 :.DWNINIRNSPPPFVPTLKSDDDTSNFDEPEKNSW.P .FSGEELPFVGFSS
 ARTDWNINIRNSPPPFVPTLKSDDDTSNFDEPEKNSWAFILCVPAEPLAFSGEELPFVGFSS

YSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKMEQEMTRLHRRVS
 YSKALG.LGRSESVVS.LDSPAK.SSMEKKLLIKSKELQDSQDKCHKMEQEMTRLHRRVS
 YSKALGYLGRSESVVSSLDSPAKVSSMEKKLLIKSKELQDSQDKCHKMEQEMTRLHRRVS

EVEAVLSQKEVELKASETQRSLLAQDLATYITECSSLKRSLEQARMEVSQEDDKALQLLH
 EVEAVLSQKEVELKASETQRSLLAQDLATYITECSSLKRSLEQARMEVSQEDDKALQLLH
 EVEAVLSQKEVELKASETQRSLLAQDLATYITECSSLKRSLEQARMEVSQEDDKALQLLH

DIREQSRKLQEIKEQEYQAQVEEMRLMMNQLEEDLVSARRRSDLYESELRESRLAAEEFK
 DIREQSRKLQEIKEQEYQAQVEEMRLMMNQLEEDLVSARRRSDLYESELRESRLAAEEFK
 DIREQSRKLQEIKEQEYQAQVEEMRLMMNQLEEDLVSARRRSDLYESELRESRLAAEEFK

RKATECQHKLKAKDQKGPEVGEYAKLEKINAEQQLKIQELQEKLEKAVKASTEATELLQ
 RKA.ECQHKL:KAKDQKGPEVGEY:KLEKINAEQQLKIQELQEKLEKAVKASTEATELLQ
 RKANECQHKLKAKDQKGPEVGEYSKLEKINAEQQLKIQELQEKLEKAVKASTEATELLQ

NIRQAKERAERELEKLQNRDSSEGIKKLVEAEERRHSLENKVKRLETMERRENRLKDD
 NIRQAKERAERELEKL.NRDSSEGI:KKLVEAEERRHSLENKVKRLETMERRENRLKDD
 NIRQAKERAERELEKLHNREDSSSEGIKKLVEAEERRHSLENKVKRLETMERRENRLKDD

IQTKSQIQQMADKILELEEKHREAQVSAQHLEVHLKQKEQHYYEKKIKVLDNQIKKDLAD
 IQTKS:QIQQMADKILELEEKHREAQVSAQHLEVHLKQKEQHYYEKKIKVLDNQIKKDLAD
 IQTKSEQIQQMADKILELEEKHREAQVSAQHLEVHLKQKEQHYYEKKIKVLDNQIKKDLAD

KETLENMMQRHEEEAHEKGKILSEQKAMINAMDSKIRSLEQRIVELSEANKLAANSSLFT
 KE:LENMMQRHEEEAHEKGKILSEQKAMINAMDSKIRSLEQRIVELSEANKLAANSSLFT
 KESLENMMQRHEEEAHEKGKILSEQKAMINAMDSKIRSLEQRIVELSEANKLAANSSLFT

QRNMKAQEEMISELRQQKFYLETQAGKLEAQNRLKEEQLEKISHQDHSDKNRLLLELETRL
 QRNMKAQEEMISELRQQKFYLETQAGKLEAQNRLKEEQLEKISHQDHSDK:RLLELETRL
 QRNMKAQEEMISELRQQKFYLETQAGKLEAQNRLKEEQLEKISHQDHSDKSRLLLELETRL

REVSLEHEEQKLELKRQLTELQLSLQERESQLTALQAARALESQLRQAKTELEETTAAE
 REVSLEHEEQKLELKRQLTELQLSLQERESQLTALQAARALESQLRQAKTELEETTAAE
 REVSLEHEEQKLELKRQLTELQLSLQERESQLTALQAARALESQLRQAKTELEETTAAE

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Fig. 8 (continued)

EEEIQALTAHRDEIQRKFDALRNSCTVITDLEEQLNQLTEDNAELNNQNFYLSKQLDEAS
EEEIQALTAHRDEIQRKFDALRNSCTVITDLEEQLNQLTEDNAELNNQNFYLSKQLDEAS
EEEIQALTAHRDEIQRKFDALRNSCTVITDLEEQLNQLTEDNAELNNQNFYLSKQLDEAS

GANDEIVQLRSEVDHLRREITEREMQLTSQKQTMEALKTTCTMLEEQVMDLEALNDELLE
GANDEIVQLRSEVDHLRREITEREMQLTSQKQTMEALKTTCTMLEEQV:DLEALNDELLE
GANDEIVQLRSEVDHLRREITEREMQLTSQKQTMEALKTTCTMLEEQVLDLEALNDELLE

KERQWEAWRSVLGDEKSQFECRVRELQRM LDTEKQSRARADQRITESRQVVELAVKEHKA
KERQWEAWRSVLGDEKSQFECRVRELQRM LDTEKQSRARADQRITESRQVVELAVKEHKA
KERQWEAWRSVLGDEKSQFECRVRELQRM LDTEKQSRARADQRITESRQVVELAVKEHKA

EILALQQALKEQKLKAESLSDKLN DLEKKHAMLEMNARSLQQKLETERELKQRLLEEQA
EILALQQALKEQKLKAESLSDKLN DLEKKHAMLEMNARSLQQKLETERELKQRLLEEQA
EILALQQALKEQKLKAESLSDKLN DLEKKHAMLEMNARSLQQKLETERELKQRLLEEQA

LQQQMDLQKNHIFRLTQGLQEALDRADLLKTERS DLEYQLENIQVLYSHEKVKMEGTISQ
LQQQMDLQKNHIFRLTQGLQEALDRADLLKTERS DLEYQLENIQVLYSHEKVKMEGTISQ
LQQQMDLQKNHIFRLTQGLQEALDRADLLKTERS DLEYQLENIQVLYSHEKVKMEGTISQ

QTKLIDFLQAKMDQPAKKKKVPLQYNELKLAL EKEKARCAELEEEALQKTRIELRSAREEA
QTKLIDFLQAKMDQPAKKKKVPLQYNELKLAL EKEKARCAELEEEALQKTRIELRSAREEA
QTKLIDFLQAKMDQPAKKKKVPLQYNELKLAL EKEKARCAELEEEALQKTRIELRSAREEA

AHRKATDHPHPSTPATARQQIAMS AIVRSPEHQPSAMSLAPPSSRRKESSTPEEFSRRL
AHRKATDHPHPSTPATARQQIAMS AIVRSPEHQPSAMSLAPPSSRRKESSTPEEFSRRL
AHRKATDHPHPSTPATARQQIAMS AIVRSPEHQPSAMSLAPPSSRRKESSTPEEFSRRL

KERMHHNIPHRFNVGLNMRATKCAVCLDTVHFGRQASKCLECQVMCHPKCSTCLPATCGL
KERMHHNIPHRFNVGLNMRATKCAVCLDTVHFGRQASKCLECQVMCHPKCSTCLPATCGL
KERMHHNIPHRFNVGLNMRATKCAVCLDTVHFGRQASKCLECQVMCHPKCSTCLPATCGL

PAEYATHFTEAFCRDKMNSPGLQTK EPSSSLHLEGWMKVPRNNKRGQQGWDRKYIVLEGS
PAEYATHFTEAFCRDKMNSPGLQ:KEP.SSLHLEGWMKVPRNNKRGQQGWDRKYIVLEGS
PAEYATHFTEAFCRDKMNSPGLQSKEPGSSSLHLEGWMKVPRNNKRGQQGWDRKYIVLEGS

KVLIYDNEAREAGQRPVEEFELCLPDGDVSIHGAVGASELANTAKADVPIILKMESH PHT
KVLIYDNEAREAGQRPVEEFELCLPDGDVSIHGAVGASELANTAKADVPIILKMESH PHT
KVLIYDNEAREAGQRPVEEFELCLPDGDVSIHGAVGASELANTAKADVPIILKMESH PHT

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Fig. 8 (continued)

TCWPGRTLYLLAPSFDPKQRWVTALESVVAGGRVSREKAEADAKLLGNSLLKLEGDDRDL
TCWPGRTLYLLAPSFDPKQRWVTALESVVAGGRVSREKAEADAKLLGNSLLKLEGDDRDL
TCWPGRTLYLLAPSFDPKQRWVTALESVVAGGRVSREKAEADAKLLGNSLLKLEGDDRDL

MNCTLPFSDQVVLVGTEEGLYALNVLKNSLTHVPGIGAVFQIYIIKDLEKLLMIAGEERA
MNCTLPFSDQVVLVGTEEGLYALNVLKNSLTH:PGIGAVFQIYIIKDLEKLLMIAGEERA
MNCTLPFSDQVVLVGTEEGLYALNVLKNSLTHIPGIGAVFQIYIIKDLEKLLMIAGEERA

LCLVDVKVKQSLAQSHLPAQPDISPNI FEAVKGCHLFGAGKIENGLCICAAMPSKVIL
LCLVDVKVKQSLAQSHLPAQPD:SPNI FEAVKGCHLF.AGKIEN.LCICAAMPSKVIL
LCLVDVKVKQSLAQSHLPAQPDVSPNI FEAVKGCHLFAAGKIENSLCICAAMPSKVIL

RYNENLSKYCIRKEIETSEPCSCIHFTNYSILIGTNKFYEIDMKQYTL EFLDKNDHSLA
RYN:NLSKYCIRKEIETSEPCSCIHFTNYSILIGTNKFYEIDMKQYTL:EFLDKNDHSLA
RYNDNLSKYCIRKEIETSEPCSCIHFTNYSILIGTNKFYEIDMKQYTLDEF LDKNDHSLA

PAVFAASSNSFPVSIVQVNSAGQREEYLLCFHEFGVFVDSYGRRSRTDDLKWSRLPLAFA
PAVFA:SSNSFPVSIVQ.NSAGQREEYLLCFHEFGVFVDSYGRRSRTDDLKWSRLPLAFA
PAVFASSNSFPVSIVQANSAGQREEYLLCFHEFGVFVDSYGRRSRTDDLKWSRLPLAFA

YREPYLFVTHFNSLEVIEIQARSSAGTPARAYLDIPNPRYLGPASSGAIYLASSYQDKL
YREPYLFVTHFNSLEVIEIQARSS.G:PARAYL:IPNPRYLGPASSGAIYLASSYQDKL
YREPYLFVTHFNSLEVIEIQARSSLGSPARAYLEIPNPRYLGPASSGAIYLASSYQDKL

RVICCKGNLVKESGTEHHRGPSTSRSSPNKRGPPPTYNEHITKRVASSPAPPEGPSHPREP
RVICCKGNLVKESGTE.HR PSTSRSSPNKRGPPPTYNEHITKRVASSPAPPEGPSHPREP
RVICCKGNLVKESGTEQHRVPSTSRSSPNKRGPPPTYNEHITKRVASSPAPPEGPSHPREP

STPHRY--REGRTelRRDKSPGRPLEREKSPGRMLSTRRERSPGRLFEDSSRGRLPAGAV
STPHRY REGRTelRRDKSPGRPLEREKSPGRMLSTRRERSPGRLFEDSSRGRLPAGAV
STPHRYRDREGRTelRRDKSPGRPLEREKSPGRMLSTRRERSPGRLFEDSSRGRLPAGAV

RTPLSQVNKVWDQSSV 2054

RTPLSQVNKVWDQSSV

RTPLSQVNKVWDQSSV 2055

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Fig. 9

BLASTP - alignment of 543_Protein against swiss|O14578|CTRO_HUMAN
 CITRON PROTEIN (FRAGMENT) ./.:treml|AC002563|AC002563_2 gene:
 "WUGSC:H_127H14.1";
 Human PAC clone 127H14 from 12q, complete sequence. ./.:gp|AC002563|2439517
 gene:
 "WUGSC:H_127H14.1"; Human PAC clone 127H14 from 12q, complete sequence.

This hit is scoring at : 0.0 (expectation value)

Alignment length (overlap) : 1286

Identities : 100 %

Scoring matrix : BLOSUM62 (used to infer consensus pattern)

Database searched : nrdb_1_;

Q: 769 VLDNQIKKDLADKETLENMMQRHEEEAHEKGKILSEQKAMINAMDSKIRSLEQRIVELSE
 VLDNQIKKDLADKETLENMMQRHEEEAHEKGKILSEQKAMINAMDSKIRSLEQRIVELSE
 H: 1 VLDNQIKKDLADKETLENMMQRHEEEAHEKGKILSEQKAMINAMDSKIRSLEQRIVELSE

ANKLAANSSLFTQRMKAQEEMISELRQQKFYLETQAGKLEAQNRLKEEQLEKISHQDHS
 ANKLAANSSLFTQRMKAQEEMISELRQQKFYLETQAGKLEAQNRLKEEQLEKISHQDHS
 ANKLAANSSLFTQRMKAQEEMISELRQQKFYLETQAGKLEAQNRLKEEQLEKISHQDHS

DKNRLLELETRLREVSLEHHEEQKLELKRQLTELQLSLQERESQLTALQAARAALESQLRQ
 DKNRLLELETRLREVSLEHHEEQKLELKRQLTELQLSLQERESQLTALQAARAALESQLRQ
 DKNRLLELETRLREVSLEHHEEQKLELKRQLTELQLSLQERESQLTALQAARAALESQLRQ

AKTELEETTAAEAEIIIQALTAHRDEIQRKFDALRNSCTVITDLEEQLNQLTEDNAELNNQ
 AKTELEETTAAEAEIIIQALTAHRDEIQRKFDALRNSCTVITDLEEQLNQLTEDNAELNNQ
 AKTELEETTAAEAEIIIQALTAHRDEIQRKFDALRNSCTVITDLEEQLNQLTEDNAELNNQ

NFYLSKQLDEASGANDEIVQLRSEVDHLRREITEREMQLTSQKQTMEALKTTCTMLEEQV
 NFYLSKQLDEASGANDEIVQLRSEVDHLRREITEREMQLTSQKQTMEALKTTCTMLEEQV
 NFYLSKQLDEASGANDEIVQLRSEVDHLRREITEREMQLTSQKQTMEALKTTCTMLEEQV

MDLEALNDELLEKERQWEAWRSVLGDEKSQFECRVRELQRMMLDTEKQSRARADQRITESR
 MDLEALNDELLEKERQWEAWRSVLGDEKSQFECRVRELQRMMLDTEKQSRARADQRITESR
 MDLEALNDELLEKERQWEAWRSVLGDEKSQFECRVRELQRMMLDTEKQSRARADQRITESR

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Fig. 9 (continued)

QVVELAVKEHKAEILALQQALKEQKLKAESLSDKLNDLEKKHAMLEMNARSLQQKLETER
QVVELAVKEHKAEILALQQALKEQKLKAESLSDKLNDLEKKHAMLEMNARSLQQKLETER
QVVELAVKEHKAEILALQQALKEQKLKAESLSDKLNDLEKKHAMLEMNARSLQQKLETER

ELKQRLLEEQAQLQQQMDLQKNHIFRLTQGLQEALDRADLLKTERSDLEYQLENIQVLYS
ELKQRLLEEQAQLQQQMDLQKNHIFRLTQGLQEALDRADLLKTERSDLEYQLENIQVLYS
ELKQRLLEEQAQLQQQMDLQKNHIFRLTQGLQEALDRADLLKTERSDLEYQLENIQVLYS

HEKVKMEGTISQQTKLIDFLQAKMDQPAKKKKVPLQYNELKLALKEKEKARCAELEEEALQK
HEKVKMEGTISQQTKLIDFLQAKMDQPAKKKKVPLQYNELKLALKEKEKARCAELEEEALQK
HEKVKMEGTISQQTKLIDFLQAKMDQPAKKKKVPLQYNELKLALKEKEKARCAELEEEALQK

TRIELRSAREEAAHRKATDHPHPSTPATARQQIAMSIVRSPEHQPSAMSLAPPSSRRK
TRIELRSAREEAAHRKATDHPHPSTPATARQQIAMSIVRSPEHQPSAMSLAPPSSRRK
TRIELRSAREEAAHRKATDHPHPSTPATARQQIAMSIVRSPEHQPSAMSLAPPSSRRK

ESSTPEEFSRRLKERMHHNIPHRFNVGLNMRATKCAVCLDTVHFGRQASKCLECQVMCHP
ESSTPEEFSRRLKERMHHNIPHRFNVGLNMRATKCAVCLDTVHFGRQASKCLECQVMCHP
ESSTPEEFSRRLKERMHHNIPHRFNVGLNMRATKCAVCLDTVHFGRQASKCLECQVMCHP

KCSTCLPATCGLPAEYATHFTEAFCDKMNPSGLQTKEPSSSLHLEGWMKVPRNNKRGQQ
KCSTCLPATCGLPAEYATHFTEAFCDKMNPSGLQTKEPSSSLHLEGWMKVPRNNKRGQQ
KCSTCLPATCGLPAEYATHFTEAFCDKMNPSGLQTKEPSSSLHLEGWMKVPRNNKRGQQ

GWDRKYIVLEGSKVLIYDNEAREAGQRPVEEFELCLPDGDVSIHGAVGASELANTAKADV
GWDRKYIVLEGSKVLIYDNEAREAGQRPVEEFELCLPDGDVSIHGAVGASELANTAKADV
GWDRKYIVLEGSKVLIYDNEAREAGQRPVEEFELCLPDGDVSIHGAVGASELANTAKADV

PYILKMESHPTHCTCWPGRTLYLLAPSFDPKQRWVTALESVVAGGRVSREKAEADAKLLGN
PYILKMESHPTHCTCWPGRTLYLLAPSFDPKQRWVTALESVVAGGRVSREKAEADAKLLGN
PYILKMESHPTHCTCWPGRTLYLLAPSFDPKQRWVTALESVVAGGRVSREKAEADAKLLGN

SLLKLEGDDRLDMNCTLPFSDQVVLVGTEEGLYALNVLKNSLTHVPGIGAVFQIYIIKDL
SLLKLEGDDRLDMNCTLPFSDQVVLVGTEEGLYALNVLKNSLTHVPGIGAVFQIYIIKDL
SLLKLEGDDRLDMNCTLPFSDQVVLVGTEEGLYALNVLKNSLTHVPGIGAVFQIYIIKDL

EKLLMIAGEERALCLVDVKKVKQSLAQSHLPAQPDISPNI FEAVKGCHLFGAGKIENGLC
EKLLMIAGEERALCLVDVKKVKQSLAQSHLPAQPDISPNI FEAVKGCHLFGAGKIENGLC
EKLLMIAGEERALCLVDVKKVKQSLAQSHLPAQPDISPNI FEAVKGCHLFGAGKIENGLC

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Fig. 9 (continued)

ICAAMPSKVILRYNENLSKYCIRKEIETSEPCSCIHFTNYSILIGTNKFYEIDMKQYTL
ICAAMPSKVILRYNENLSKYCIRKEIETSEPCSCIHFTNYSILIGTNKFYEIDMKQYTL
ICAAMPSKVILRYNENLSKYCIRKEIETSEPCSCIHFTNYSILIGTNKFYEIDMKQYTL

EEFLDKNDHSLAPAVFAASSNSFPVSIVQVNSAGQREEYLLCFHEFGVFVDSYGRRSRD
EEFLDKNDHSLAPAVFAASSNSFPVSIVQVNSAGQREEYLLCFHEFGVFVDSYGRRSRD
EEFLDKNDHSLAPAVFAASSNSFPVSIVQVNSAGQREEYLLCFHEFGVFVDSYGRRSRD

DLKWSRLPLAFAYREPYLFVTHFNSLEVIEIQARSSAGTPARAYLDIPNPRYLGPASSG
DLKWSRLPLAFAYREPYLFVTHFNSLEVIEIQARSSAGTPARAYLDIPNPRYLGPASSG
DLKWSRLPLAFAYREPYLFVTHFNSLEVIEIQARSSAGTPARAYLDIPNPRYLGPASSG

AIYLASSYQDKLRVICCKGNLVKESGTEHHRGPSTSRSSPNKRGPPPTYNEHITKRVASSP
AIYLASSYQDKLRVICCKGNLVKESGTEHHRGPSTSRSSPNKRGPPPTYNEHITKRVASSP
AIYLASSYQDKLRVICCKGNLVKESGTEHHRGPSTSRSSPNKRGPPPTYNEHITKRVASSP

APPEGPSHPREPSTPHRYREGRTTELRRDKSPGRPLEREKSPGRMLSTRRERSPGRLFEDS
APPEGPSHPREPSTPHRYREGRTTELRRDKSPGRPLEREKSPGRMLSTRRERSPGRLFEDS
APPEGPSHPREPSTPHRYREGRTTELRRDKSPGRPLEREKSPGRMLSTRRERSPGRLFEDS

SRGRLPAGAVRTPLSQVNKVWDQSSV 2054
SRGRLPAGAVRTPLSQVNKVWDQSSV
SRGRLPAGAVRTPLSQVNKVWDQSSV 1286

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Fig. 10

BLASTP - alignment of 543_Protein against aageneseq|AAB43359|AAB43359
Human ORFX ORF3123 polypeptide sequence SEQ ID NO:6246.

This hit is scoring at : 0.0 (expectation value)
Alignment length (overlap) : 1286
Identities : 100 %
Scoring matrix : BLOSUM62 (used to infer consensus pattern)
Database searched : aageneseq

Q: 769 VLDNQIKKDLADKETLENMMQRHEEEAHEKGKILSEQKAMINAMDSKIRSLEQRIVELSE
VLDNQIKKDLADKETLENMMQRHEEEAHEKGKILSEQKAMINAMDSKIRSLEQRIVELSE
H: 1 VLDNQIKKDLADKETLENMMQRHEEEAHEKGKILSEQKAMINAMDSKIRSLEQRIVELSE

ANKLAANSSLFTQRNMKAQEEMISELRQOKFYLETQAGKLEAQNRKLEEQLEKISHQDHS
ANKLAANSSLFTQRNMKAQEEMISELRQOKFYLETQAGKLEAQNRKLEEQLEKISHQDHS
ANKLAANSSLFTQRNMKAQEEMISELRQOKFYLETQAGKLEAQNRKLEEQLEKISHQDHS

DKNRLLELETRLREVSLEHEEQKLELKRQLTELQLSLQERESQLTALQAARAALESQLRQ
DKNRLLELETRLREVSLEHEEQKLELKRQLTELQLSLQERESQLTALQAARAALESQLRQ
DKNRLLELETRLREVSLEHEEQKLELKRQLTELQLSLQERESQLTALQAARAALESQLRQ

AKTELEETTAAEIEEEIQALTAHRDEIQRKFDALRNSCTVITDLEEQLNQLTEDNAELNNQ
AKTELEETTAAEIEEEIQALTAHRDEIQRKFDALRNSCTVITDLEEQLNQLTEDNAELNNQ
AKTELEETTAAEIEEEIQALTAHRDEIQRKFDALRNSCTVITDLEEQLNQLTEDNAELNNQ

NFYLSKQLDEASGANDEIVQLRSEVDHLRREITEREMQLTSQKQTMEALKTTCTMLEEQV
NFYLSKQLDEASGANDEIVQLRSEVDHLRREITEREMQLTSQKQTMEALKTTCTMLEEQV
NFYLSKQLDEASGANDEIVQLRSEVDHLRREITEREMQLTSQKQTMEALKTTCTMLEEQV

MDLEALNDELLEKERQWEAWRSVLGDEKSQFECRVRELQRM LDTEKQSRARADQRITESR
MDLEALNDELLEKERQWEAWRSVLGDEKSQFECRVRELQRM LDTEKQSRARADQRITESR
MDLEALNDELLEKERQWEAWRSVLGDEKSQFECRVRELQRM LDTEKQSRARADQRITESR

QVVELAVKEHKAEILALQQALKEQKLKAESLSDKLN DLEKKHAMLEMNARSLQQKLETER
QVVELAVKEHKAEILALQQALKEQKLKAESLSDKLN DLEKKHAMLEMNARSLQQKLETER
QVVELAVKEHKAEILALQQALKEQKLKAESLSDKLN DLEKKHAMLEMNARSLQQKLETER

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Fig. 10 (continued)

ELKQRLLEEQA KLQQQMDLQKNHIFRLTQGLQEALDRADLLKTERS DLEYQLENIQVLYS
ELKQRLLEEQA KLQQQMDLQKNHIFRLTQGLQEALDRADLLKTERS DLEYQLENIQVLYS
ELKQRLLEEQA KLQQQMDLQKNHIFRLTQGLQEALDRADLLKTERS DLEYQLENIQVLYS

HEKVMEGTISQQTKLIDFLQAKMDQPAKKKKVPLQYNELKLAL EKEKARCAELEEEALQK
HEKVMEGTISQQTKLIDFLQAKMDQPAKKKKVPLQYNELKLAL EKEKARCAELEEEALQK
HEKVMEGTISQQTKLIDFLQAKMDQPAKKKKVPLQYNELKLAL EKEKARCAELEEEALQK

TRIELRSAREEAAHRKATDHPHPSTPATARQQIAMS AIVRSPEHQPSAMSL LAPPSSRRK
TRIELRSAREEAAHRKATDHPHPSTPATARQQIAMS AIVRSPEHQPSAMSL LAPPSSRRK
TRIELRSAREEAAHRKATDHPHPSTPATARQQIAMS AIVRSPEHQPSAMSL LAPPSSRRK

ESSTPEEFSRRLKERMHHNIPHRFNVGLNM RATKCAVCLDTVHFGRQASKCLECQVMCHP
ESSTPEEFSRRLKERMHHNIPHRFNVGLNM RATKCAVCLDTVHFGRQASKCLECQVMCHP
ESSTPEEFSRRLKERMHHNIPHRFNVGLNM RATKCAVCLDTVHFGRQASKCLECQVMCHP

KCSTCLPATCGLPAEYATHFTEAFCDKMNSPGLQTKEPSSSLHLEGWMKVPRNNKRGQQ
KCSTCLPATCGLPAEYATHFTEAFCDKMNSPGLQTKEPSSSLHLEGWMKVPRNNKRGQQ
KCSTCLPATCGLPAEYATHFTEAFCDKMNSPGLQTKEPSSSLHLEGWMKVPRNNKRGQQ

GWDRKYIVLEGSKVLIYDNEAREAGQRPVEEFELCLPDGDVSIHGAVGASELANTAKADV
GWDRKYIVLEGSKVLIYDNEAREAGQRPVEEFELCLPDGDVSIHGAVGASELANTAKADV
GWDRKYIVLEGSKVLIYDNEAREAGQRPVEEFELCLPDGDVSIHGAVGASELANTAKADV

PYILKMESH PHTTCWPGR TLYLLAPSFPDKQRWVTALESVVAGGRVSREKAEADAKLLGN
PYILKMESH PHTTCWPGR TLYLLAPSFPDKQRWVTALESVVAGGRVSREKAEADAKLLGN
PYILKMESH PHTTCWPGR TLYLLAPSFPDKQRWVTALESVVAGGRVSREKAEADAKLLGN

SLLKLEGDDR LDMNCTLPFSDQVVLVGTEEGLYALNVLKNSLTHVPGIGAVFQIYI IKDL
SLLKLEGDDR LDMNCTLPFSDQVVLVGTEEGLYALNVLKNSLTHVPGIGAVFQIYI IKDL
SLLKLEGDDR LDMNCTLPFSDQVVLVGTEEGLYALNVLKNSLTHVPGIGAVFQIYI IKDL

EKLLMIAGEERALCLVDVKKVKQSLAQSHLPAQPDISPNI FEAVKGCHLFGAGKIENGLC
EKLLMIAGEERALCLVDVKKVKQSLAQSHLPAQPDISPNI FEAVKGCHLFGAGKIENGLC
EKLLMIAGEERALCLVDVKKVKQSLAQSHLPAQPDISPNI FEAVKGCHLFGAGKIENGLC

ICAAMPSKV VILRYNENLSKYCIRKEIETSEPCSCIHFTNYSILIGTNKFYEIDMKQYTL
ICAAMPSKV VILRYNENLSKYCIRKEIETSEPCSCIHFTNYSILIGTNKFYEIDMKQYTL
ICAAMPSKV VILRYNENLSKYCIRKEIETSEPCSCIHFTNYSILIGTNKFYEIDMKQYTL

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Fig. 10 (continued)

EEFLDKNDHSLAPAVFAASSNSFPVSIVQVNSAGQREEYLLCFHEFGVFVDSYGRRSRD
EEFLDKNDHSLAPAVFAASSNSFPVSIVQVNSAGQREEYLLCFHEFGVFVDSYGRRSRD
EEFLDKNDHSLAPAVFAASSNSFPVSIVQVNSAGQREEYLLCFHEFGVFVDSYGRRSRD

DLKWSRLPLAFAYREPYLFVTHFNSLEVIEIQARSSAGTPARAYLDIPNPRYLGPASSG
DLKWSRLPLAFAYREPYLFVTHFNSLEVIEIQARSSAGTPARAYLDIPNPRYLGPASSG
DLKWSRLPLAFAYREPYLFVTHFNSLEVIEIQARSSAGTPARAYLDIPNPRYLGPASSG

AIYLASSYQDKLRVICCKGNLVKESGTEHHRGPSTSRSSPNKRGPPPTYNEHITKRVASSP
AIYLASSYQDKLRVICCKGNLVKESGTEHHRGPSTSRSSPNKRGPPPTYNEHITKRVASSP
AIYLASSYQDKLRVICCKGNLVKESGTEHHRGPSTSRSSPNKRGPPPTYNEHITKRVASSP

APPEGPSHPREPSTPHRYREGRTTELRRDKSPGRPLEREKSPGRMLSTRRERSPGRLFEDS
APPEGPSHPREPSTPHRYREGRTTELRRDKSPGRPLEREKSPGRMLSTRRERSPGRLFEDS
APPEGPSHPREPSTPHRYREGRTTELRRDKSPGRPLEREKSPGRMLSTRRERSPGRLFEDS

SRGRLPAGAVRTPLSQVNKVWDQSSV 2054
SRGRLPAGAVRTPLSQVNKVWDQSSV
SRGRLPAGAVRTPLSQVNKVWDQSSV 1286

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Fig. 11

BLASTP - alignment of 543_Protein against trembl|AB023166|AB023166_1
 gene: "KIAA0949"; product: "KIAA0949 protein"; Homo sapiens mRNA for
 KIAA0949
 protein, partial cds. //:gp|AB023166|4589542 gene: "KIAA0949"; product:
 "KIAA0949 protein"; Homo sapiens mRNA for KIAA0949 protein, partial cds.

This hit is scoring at : 0.0 (expectation value)

Alignment length (overlap) : 940

Identities : 100 %

Scoring matrix : BLOSUM62 (used to infer consensus pattern)

Database searched : nrdb_1_;

Q: 1115 QSRARADQRITESRQVVELAVKEHKAETILALQQALKEQKLKAESLSDKLNDEKKHAMLE
 QSRARADQRITESRQVVELAVKEHKAETILALQQALKEQKLKAESLSDKLNDEKKHAMLE
 H: 1 QSRARADQRITESRQVVELAVKEHKAETILALQQALKEQKLKAESLSDKLNDEKKHAMLE

MNARSLQQKLETERELKQRLLEEQAKLQQQMDLQKNHIFRLTQGLQEALDRADLLKTERS
 MNARSLQQKLETERELKQRLLEEQAKLQQQMDLQKNHIFRLTQGLQEALDRADLLKTERS
 MNARSLQQKLETERELKQRLLEEQAKLQQQMDLQKNHIFRLTQGLQEALDRADLLKTERS

DLEYQLENIQVLYSHEKVMEGTISQQTKLIDFLQAKMDQPAKKKKVPLQYNELKLALEK
 DLEYQLENIQVLYSHEKVMEGTISQQTKLIDFLQAKMDQPAKKKKVPLQYNELKLALEK
 DLEYQLENIQVLYSHEKVMEGTISQQTKLIDFLQAKMDQPAKKKKVPLQYNELKLALEK

EKARCAELEEEALQKTRIELRSAREEEAHRKATDHPHPSTPATARQQIAMSIVRSPEHQ
 EKARCAELEEEALQKTRIELRSAREEEAHRKATDHPHPSTPATARQQIAMSIVRSPEHQ
 EKARCAELEEEALQKTRIELRSAREEEAHRKATDHPHPSTPATARQQIAMSIVRSPEHQ

SAMSLAPPSSRRKESSTPEEFSRRLKERMHHNI PHRFNVGLNMRATKCAVCLDTVHFG
 SAMSLAPPSSRRKESSTPEEFSRRLKERMHHNI PHRFNVGLNMRATKCAVCLDTVHFG
 SAMSLAPPSSRRKESSTPEEFSRRLKERMHHNI PHRFNVGLNMRATKCAVCLDTVHFG

QASKCLECQVMCHPKCSTCLPATCGLPAEYATHFTEAFCDKMNSPGLQTKEPSSSLHLE
 QASKCLECQVMCHPKCSTCLPATCGLPAEYATHFTEAFCDKMNSPGLQTKEPSSSLHLE
 QASKCLECQVMCHPKCSTCLPATCGLPAEYATHFTEAFCDKMNSPGLQTKEPSSSLHLE

GWMKVPRNNKRGQQGWRKYIVLEGSKVLIYDNEAREAGQRPVEEFELCLPDGDVSIHGA
 GWMKVPRNNKRGQQGWRKYIVLEGSKVLIYDNEAREAGQRPVEEFELCLPDGDVSIHGA
 GWMKVPRNNKRGQQGWRKYIVLEGSKVLIYDNEAREAGQRPVEEFELCLPDGDVSIHGA

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Fig 11 (continued)

VGASELANTAKADVPIILKMESHPTTCWPGRTLYLLAPSFPDKQRWVTALESVVAGGRV
VGASELANTAKADVPIILKMESHPTTCWPGRTLYLLAPSFPDKQRWVTALESVVAGGRV
VGASELANTAKADVPIILKMESHPTTCWPGRTLYLLAPSFPDKQRWVTALESVVAGGRV

SREKAEADAKLLGNSLLKLEGDDRDLDMNCTLPFSDQVVLVGTEEGLYALNVLKNSLTHVP
SREKAEADAKLLGNSLLKLEGDDRDLDMNCTLPFSDQVVLVGTEEGLYALNVLKNSLTHVP
SREKAEADAKLLGNSLLKLEGDDRDLDMNCTLPFSDQVVLVGTEEGLYALNVLKNSLTHVP

GIGAVFQIYIIKDLEKLLMIAGEERALCLVDVKKVKQSLAQSHLPAQPDISPNI FEAVKG
GIGAVFQIYIIKDLEKLLMIAGEERALCLVDVKKVKQSLAQSHLPAQPDISPNI FEAVKG
GIGAVFQIYIIKDLEKLLMIAGEERALCLVDVKKVKQSLAQSHLPAQPDISPNI FEAVKG

CHLFGAGKIEGLCICAAMPSKVILRYNENLSKYCIRKEIETSEPCSCIHFTNYSILIG
CHLFGAGKIEGLCICAAMPSKVILRYNENLSKYCIRKEIETSEPCSCIHFTNYSILIG
CHLFGAGKIEGLCICAAMPSKVILRYNENLSKYCIRKEIETSEPCSCIHFTNYSILIG

TNKFYEIDMKQYTLEEFLDKNDHSLAPAVFAASSNSFPVSIVQVNSAGQREEYLLCFHEF
TNKFYEIDMKQYTLEEFLDKNDHSLAPAVFAASSNSFPVSIVQVNSAGQREEYLLCFHEF
TNKFYEIDMKQYTLEEFLDKNDHSLAPAVFAASSNSFPVSIVQVNSAGQREEYLLCFHEF

GVFVDSYGRRSRTDDLKWSRLPLAFAYREPYLFVTHFNSLEVIEIQARSSAGTPARAYLD
GVFVDSYGRRSRTDDLKWSRLPLAFAYREPYLFVTHFNSLEVIEIQARSSAGTPARAYLD
GVFVDSYGRRSRTDDLKWSRLPLAFAYREPYLFVTHFNSLEVIEIQARSSAGTPARAYLD

IPNPRYLGPASSGAIYLASSYQDKLRVICCKGNLVKESGTEHHRGPSTSRSSPNKRGP
IPNPRYLGPASSGAIYLASSYQDKLRVICCKGNLVKESGTEHHRGPSTSRSSPNKRGP
IPNPRYLGPASSGAIYLASSYQDKLRVICCKGNLVKESGTEHHRGPSTSRSSPNKRGP

TYNEHITKRVASSPAPPEGPSHPREPSTPHRYREGRTTELRRDKSPGRPLEREKSPGRMLS
TYNEHITKRVASSPAPPEGPSHPREPSTPHRYREGRTTELRRDKSPGRPLEREKSPGRMLS
TYNEHITKRVASSPAPPEGPSHPREPSTPHRYREGRTTELRRDKSPGRPLEREKSPGRMLS

TRRERSPGRLFEDSSRGRLPAGAVRTPLSQVNKVWDQSSV 2054
TRRERSPGRLFEDSSRGRLPAGAVRTPLSQVNKVWDQSSV
TRRERSPGRLFEDSSRGRLPAGAVRTPLSQVNKVWDQSSV 940

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Fig. 12

BLASTP - alignment of 543_Protein against swissnew|P54265|DMK_MOUSE
 MYOTONIN-PROTEIN KINASE (EC 2.7.1.-) (MYOTONIC DYSTROPHY PROTEIN KINASE) (MDPK)
 (DM-KINASE) (DMK) (DMPK) (MT-PK).//:swiss|P54265|DMK_MOUSE MYOTONIN-PROTEIN
 KINASE
 (EC 2.7.1.-) (MYOTONIC DYSTROPHY PROTEIN KINASE) (MDPK) (DM-KINASE) (DMK) (DMPK)
 (MT-PK).//:treml|Z38015|MMMDMPK_1 gene: "DM-PK"; product: "myotonic dystrophy
 protein kinase"; M.musculus DMR-N9 gene, exons 4 and 5, and DM-PK gene encoding
 myotonic dystrophy protein kinase //:gp|Z38015|563526 gene: "DM-PK"; product:
 "myotonic dystrophy protein kinase"; M.musculus DMR-N9 gene, exons 4 and 5, and
 DM-PK gene encoding myotonic dystrophy protein kinase.

This hit is scoring at : 3e-89 (expectation value)

Alignment length (overlap) : 522

Identities : 38 %

Scoring matrix : BLOSUM62 (used to infer consensus pattern)

Database searched : nrdb_1_;

Q: 46 LSREGILDALFVLFEBCSQPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGC
 L. E :LD.L. ::E.... L.: K:V::F::A.L:E:: ...DFE: ::G
 H: 20 LGLEPLDLLLLGVHQELGASHLAQDKYVADFLQWVEPIAARLKEVRLQRDDFEILKVIGR

GHFAEVQVVREKATGDIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQ
 G F:EV.VV: K.TG.:YAMK:M.K :L.: :VS F.EER::L ... WI.QL.:AFQ
 GAFSEVAVVKMKQTGQVYAMKIMNKWDMLKRGEVSCFREERDVLVKGDRRWITQLHFAFQ

DKNHLYLVMEYQPGDLLSLLNRYEDQLDENLIQFYLAELILAVHSVHLMGYVHRDIKPE
 D:N:LYLVMEY. GGDLL:LL::: :::::FYLAE:::A:.SVH :GYVHRDIKP:
 DENYLYLVMEYVGGDLLTLLSKFGERIPAEMARFYLAEIVMAIDSVHRLGYVHRDIKPD

NILVDRTGHIKLVDFGSAKMNSNMVNAKLPIGTPDYMAPEVL-TVMNGDGKGTYGLDC
 NIL:DR.GHI:L.DFGS..K::: MV.: ::GTPDY::PE:L .V .G.G.G:YG :C
 NILLDRCGHIRLADFGSCLKLQPDGMVRSLSVAVGTPDYLSPEILQAVGGGPGAGSYGPEC

DWWSVGVIAYEMIYGRSPFAEGTSARTFNNIMNFQRFLKFP-DDPKVSSDFLDLIQSLLC
 DWW::GV.AYEM.YG::PF ::::A.T: .I:::..L..P D. V.: DLI:.LLC
 DWWALGVFAYEMFYGQTPFYADSTAETYAKIVHYREHLSLPLADTVVPPEEAQDLIRGLLC

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Fig. 12 (continued)

GQKERLKFEG---LCCHPFFSKIDWNNIRNSPPPFVPTLKSDDDTSNFD--EPEKNSWVS
.: RL G . HPFF :DW...:R:S PPF.P.... .DT.NFD E...:VS
PAEIRLGRGGAGDFQKHPFFFGLDWEGLRDSVPPFTPDPFEGATDTCNFDVVEDRLTAMVS

SSPCQLSPSGFS---GEELPFVGFSYSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKS
.. .LS.. . G .LPFVG:SY . :. R...V P .T.. :.L :.
GGGETLSDMQEDMPLGVRLPFVGYSY---CCMAFRDNQV-----PDPTPMELEALQLPV

KELQDSQDKCHKMEQEMTRLHRRVSEVEAVLSQKEVELKASETQRSLLLEQDLATYITECS
.:LQ. . : : .V.A :...E.....Q.:L E: L.. .
SDLQGLDLQPPVSPPDQVAEEADLVAVPAPVAEATTVTLQQLQEALEEEVLTR-----Q

SLKRSLE---QARMEVSQEDDKALQLLHDIREQSRKLQEIKE 554
SL.R.LE .A....S.: :A .D:... R:LQE .E
SLSRELEAIRTANQNFSQLQEA EVNRDLEAHVRQLQERME 527

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Fig. 13

BLASTP - alignment of 543_Protein against pdb|1CDK|1CDK-A

camp-dependent protein kinase (protein kinase a) protein kinase
inhibitor (pki(5-24))

This hit is scoring at : 4e-44 (expectation value)

Alignment length (overlap) : 333

Identities : 33 %

Scoring matrix : BLOSUM62 (used to infer consensus pattern)

Database searched : nrdb_1_;

```

Q:      71 KHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCCHFAEVQVVREKATGDIYAMKVMKK
      K  .:F::K::.....L.   .FE  .::G.G.F..V.:V:.K.TG: :AMK::K
H:      14 KAKEDFLKKWENPAQNTAHL-----QFERIKTLGTGSFGRVMLVKHKETGNHFMKILDK

      KALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLVLMHEYQPGGDLSSLNRYE
      :...:Q:...  .E:.IL...  .P:::L:Y:F:D::LY:VMEY PGG::S L.R.
      QKVVKLKQIEHTLNEKRILQAVNFPFLVKLEYSFKDNSNLYMVMEYVPGGEMFSLRRI-

      DQLDENLIQFYLAELILAVHSVHLMGYVHRDIKPENILVDRTGHIKLVDFGSAAKMNSNK
      ....E  .:FY.A::L...  :H  ::::RD:KPEN:L:D:.G:I::DFG A:::....
      GRFSEPHARFYAAQIVLTFEYLHSLDLIYRDLKPENLLIDQQGYIQVTDFGFAKRVKGRT

      MVNAKLPIGTPDYMAPEVLTVMNGDGKGTYGLDCDWWSVGVIAYEMIYGRSPFAEGTSAR
      ..  .  GTP:Y:APE::..  .KG Y.  .DWW::GV:.YEM. G .PF .....:
      WTLC----GTPEYLAPEIIL-----SKG-YNKAVDWWALGVLIYEMAAGYPPFFADQPIQ

      TFNNIMNFQRFLKFPDDPKVSSDFLDLIQSLLCGQKERLKFEG-----LCCHPFFSK
      ....I:::  ::FP.  ..SSD. DL:::LL  Q : .K  G  :  H.:F:.
      IYEKIVSGK--VRFPS--HFSSDLKDLLRNLL--QVDLTKRFGNLKDGVNNDIKNHKWFAT

      IDWNNI--RNSPPPFVPTLKSDDDTSNFDEPEK      393
      .DW  I  R.  ..PF:P..K...DTSNFD: E:
      TDWIAIYQRKVEAPFIPKFKGPGDTSNFDDYEE      325

```


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Fig. 14

HMMPFAM - alignment of 543_Protein against pfam|hmm|kinase
Protein kinase domain

This hit is scoring at : 219.4 E=5.5e-62

Scoring matrix : BLOSUM62 (used to infer consensus pattern)

```

Q:      97 FEVRSLVGCGHFAEVQVVREKaTGDIYAMKVMKKKALLaqeqvsffEEEERNILSRSTSPW
      :E:  . :G G.F.:V. ...K TG.I.A:K::KK::L          .E .IL.R :.P
H:      1 yelleklGeGsfgGkVykakhk.tgkivAvKilkkels.....lrEiqilkrIsHpN

      IPQLQYAFQ-DKNHLYLVMEYQPGGDLSSLNRYEdQLDENLIQFYLAELILAVHSVHLM
      I :L .F: ..:HLYLVMEY..GGDL...L.R   .L.E. ..: ..::: ..: :H
      IvrlIgvfedtdhhlylvMEymegGdLfdylrrng.plsekeakkialQilrGleYLHsn

      GYVHRDIKPENILVDRTGHIKLVDFGSAAKMnsnkmVNAKLPIGTPDYM-APEVltvMNG
      G.VHRD:KPENIL:D..G :K:.DFG A. :      .... :GTP YM APEV: ..G
      givHRDLKpeNILldengtvKiaDFGLArll.....eklttfvGTpwYmmAPEvi..leg

      dgkGTYGLDCDWWSVGVIAYEMIYG-----RSPFAE---
      Y. ..D WS:GVI.YE:: G                      : PF::
      ...rgysskvDvWSlGviLyElItggplfpgadlpftggdevdqliifvklPfsdelp

      ----GTSARTFNNIMNfqrflKFPDDPKVSSDFLDLIQSLLC-GQKERL---KFEGLCCH
      .. ...F. ..      :.P ....S... DL:...L   ...:R   . : :. H
      ktridpleelfrikkr.....rlplpsncSeelkdLlkkcLnkDPskRpGsatakeilnh

PFF      360
P:F
pwf      278

```

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Fig. 15

HMMPFAM - alignment of 543_Protein against pfam|hmm|PH
PH domain

This hit is scoring at : 45.8 E=1.8e-11

Scoring matrix : BLOSUM62 (used to infer consensus pattern)

Q: 1471 LHLEGWMKVPRnnkrgqQGWD RKYIVLEGSKVLIYDNE-AREAGQRPVEEFELCLpDGdv
: EGW: .. :.W.:Y.VL .: :L.Y...G. P:. :.
H: 1 vikeGwLlkks.....kswkkRyfvLfnnvLllykdskkkpkgsipLsgcqvek.pd..

sihgavgaselantakadvPYILKMEShPHttcwpgrTLYLLAPSFPDKQRWVTALESVV
. : . TL.L A.S WV.A::S.:
.....kncFeirt.dr.....tlllqaeseeerkeWvkaiqsai

A 1590

.

r 85

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Fig. 16

HMMPFAM - alignment of 543_Protein against pfam|hmm|CNH

CNH domain (Domain found in NIK1-like kinase, mouse citron and yeast ROM1, ROM2)

This hit is scoring at : 380.7 1.5e-110

Scoring matrix : BLOSUM62 (used to infer consensus pattern)

Q: 1619 LDMNCTLPFSDQ-----VVLVGTEEGLYALNVLKN-----SLTHVPGIGAVFQIYII
C. P.: . :LVGTEEGLY.LN: .. :L.: . :V QI:::
 H: 1 ytakcnhpitcdalWGkiLLvgTeeGLYvlnisdqlnkdhfegtlekiisrrsvtqiwvl

KDLEKLLMIAGE---ERALCLVDVKV-----KQSLAQSHLPAQPDISPNIIEA
 :: . LLMI:G: A L .: : K.:L...L .: .: . E
 eennvLlmisGkppylyahpLsglvekklaqknspisikdalgsarlviRknvlsvkied

VKG--CHLFGA-GKIEN--GLCICAAMPSKVIL--RYNENLSKYCIR-----
 VKG CHLF.. .: L :.AA:.S.V :L YN. . .:
 vkGNSchl favkvngkragilflaaalkssvqllaqwynplkkfklfksSNNiLNNEled

-----KEIETSEPCSCIHFTNY---SILIGTNK---FYEIDMKQYTL-----E
 K I . . . : : .I.IG.:K .D: Q: .
 ikkflkklivpvpllvveltsssfelpkiciGvdkPVGgeagfdvvqfhqtphlNslkfks

EFLDKNDHSLAPAVFAASS-----NSFPVSIVQVNSAGQREEYLLCFHEFGVFVDSYG--
K.D SL. A: ..S.V IVQ :..GQR:E.LLCF.EFGVFV: .G
 slvskedlslpnaleetskkiaTCkpisviivqqsdgGqRdelLLcfdefgvfVNlqGae

-RRSRTDDLKWSRLPLAFAYREPYLFVTHFNSLEVIEIQARSS-AGTPARA-YLDIPNPR
 RRSR.. L.W. :P AFAY EPYL.. H N.:E: EI:. . . A . .L:. . R
 arrsrkpiltwefmpeafayvepyllafhsngieIreietgelNlqeladralllearkir

YLGP-AISSGAIYLASSY 1916
 .LG. .IS. .I.L:SS
 lLgsCeisdrkIllsssp 378

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Fig. 17

HMMPFAM - alignment of 543_Protein against pfam|hmm|DAG_PE-bind
Phorbol esters/diacylglycerol binding

This hit is scoring at : 28.7 E=6.1e-05

Scoring matrix : BLOSUM62 (used to infer consensus pattern)

```
Q: 1390 HRFNVGLN-MRATKCAVCLDTVHFG-RQASKCLECQVMCHPKCSTCLPATC 1438
      HRF. . ...T C C :: :Q. KC .C : .H.:C.. :P..C
H: 1 HrFkrttfyksptfCdhCgellwglakQGlkCsnCglnvHkrChekVptnC 51
```

Note: Phorbol esters/diacylglycerol binding domain also as the Protein kinase C conserved region 1 (C1) domain. Diacylglycerol (DAG) is an important second messenger. Phorbol esters (PE) are analogues of DAG and potent tumor promoters that cause a variety of physiological changes when administered to both cells and tissues. DAG activates a family of serine/threonine protein kinases, collectively known as protein kinase C (PKC). Phorbol esters can directly stimulate PKC. The N-terminal region of PKC, known as C1, has been shown to bind PE and DAG in a phospholipid and zinc-dependent fashion. The C1 region contains one or two copies (depending on the isozyme of PKC) of a cysteine-rich domain about 50 amino-acid residues long and essential for DAG/PE-binding.

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Fig. 18

HMMPFAM - alignment of 543_Protein against pfam|hmm|pkinase_C
Protein kinase C terminal domain

This hit is scoring at : 15.4 E=0.0018

Scoring matrix : BLOSUM62 (used to infer consensus pattern)

```
Q:      361 SKIDWNNI--RNSPPPFVPTLKSDDDTSNFDE      390
          .:IDW:::  :. .PPF P.:KS. DTSNFD:
H:       1 reIdWdkLEnkeiePPFKPkiksprDtsNFDk      32
```

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Fig. 19

Prosites results:

PS00479	1390->1439	DAG_PE_BIND_DOM_1	PDOC00379
PS00029	854->876	LEUCINE_ZIPPER	PDOC00029
PS00029	991->1013	LEUCINE_ZIPPER	PDOC00029
PS00029	1057->1079	LEUCINE_ZIPPER	PDOC00029
PS00029	1159->1181	LEUCINE_ZIPPER	PDOC00029
PS00107	103->127	PROTEIN_KINASE_ATP	PDOC00100
PS00108	217->230	PROTEIN_KINASE_ST	PDOC00100
PS00867	1172->1180	CPSASE_2	PDOC00676

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Fig. 20

genewise output:

```

gi|3599509|gb|A      1 MLKFKYGVRNPPEASASEPIASRASRLNLFFQ
                      MLKFKYG RNP +A A+EPIASRASRLNLFFQ
                      MLKFKYGARNPLDAGAAEPIASRASRLNLFFQ
gi|13653116|r1909637 atatatggcactggggggcagacgtacacttc
                      ttataagcgactacgccactcggccgtatttta
                      gggcataggttggttttactccgccggtgccg

gi|3599509|gb|A      33                      GKPPPLMTQQQMSALSREGMLDALFAL
                      GKPP MTQQQMS LSREG+LDALF L
                      GKPPFMTQQQMSPLSREGILDALFVL
gi|13653116|r1909733 GTAACAG Intron 1 TAGgacctaaccctcctcggtggctgc
                      0-----[1909733:1916-0>gaccttcaaatacctcgagttactttt
                      gaactgtagggtttcaagaatccttc

gi|3599509|gb|A      59 FEECSQPALMKMKHVSSFVQK                      SD
                      FEECSQPALMK+KHVS+FV+K                      SD
                      FEECSQPALMKIKHVSNFVRK                      Y:Y[tat]          SD
gi|13653116|r1916682 tggtagcgcaaaacgaatgcatGTAAGTT Intron 2 CAGATtg
                      taaggaccttataatgattga 1-----[1916746:1928-1> ca
                      taactgttggtggtgcgcctcgg                      cc

gi|3599509|gb|A      83 TIAELRELQPSARDFEVRSLVGC GHFAEVQVVREKATGDVYAMKIMKKK
                      TIAEL+ELQPSA+DFEVRSLVGC GHFAEVQVVREKATGD+YAMK+MKKK
                      TIAELQELQPSAKDFEVRSLVGC GHFAEVQVVREKATGDIYAMKVMKKK
gi|13653116|r1928115 aaggtcgccctgagtgaacggtgctgggaggagagaggatgaagaaaa
                      ctcataatacccaatatggttgggatcatattgaaccgataactattaa
                      catgagggcgtgagccacattatttcttagggaagaacgccttgaggggg

gi|3599509|gb|A      132 ALLAQEQ                      VSFFEEERNILSRSTSPWI
                      ALLAQEQ                      VSFFEEERNILSRSTSPWI
                      ALLAQEQ                      VSFFEEERNILSRSTSPWI

```

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Fig. 20 (continued)

gi|13653116|r1928262 gttgcgcGTAGGAG Intron 3 TAGgtttgggcaattcaaacta
 cttcaaa0-----[1928283:1935-0>tcttaaagattcggcgcgt
 tagcggg tattgaggcaatacacggc

gi|3599509|gb|A 158 PQLQYAFQDKNNLYL VMEYQPGGDFL
 PQLQYAFQDKN+LYL VMEYQPGGD+L
 PQLQYAFQDKNHLYL VMEYQPGGDLL
 gi|13653116|r1935587 cctctgtcgaacctcGTGAGTC Intron 4 CAGgagtcggggtc
 cataactaaaaatat0-----[1935632:1951-0>ttaaaccgatt
 caagtctgcatcttg cgatgtagcgg

gi|3599509|gb|A 184 SLLNRYEDQLDESMIQFYLAELILAVHSVHMGYVH
 SLLNRYEDQLDE++IQFYLAELILAVHSVH MGYVH
 SLLNRYEDQLDENLIQFYLAELILAVHSVHLMGYVH
 gi|13653116|r1951610 tctaattggctggacacttcggcatggcagccagtgc
 cttagaaaataaattatatcatttctagtattgata
 atgtatgcgatacgagtcatgggtgttccttggacgt

gi|3599509|gb|A 220 DIKPENILIDRTGEIKLVDFGSA
 DIKPENIL+DRTG IKLVDFGSA
 R:R[cga] DIKPENILVDRTGHIKLVDFGSA
 gi|13653116|r1951718 CGGTAAGTG Intron 5 CAGAgaacgaacggcagcaacggtgtg
 2-----[1951720:1952-2> atacaatttagcgatattatgcc
 ccgtgctctccaaccgggttatc

gi|3599509|gb|A 244 AKMNSNKV -DAKLPIGTPDYMAPEVL
 AKMNSNK+ AKLPIGTPDYMAPEVL
 AKMNSNKM VNAKLPIGTPDYMAPEVL
 gi|13653116|r1953011 gaaataaaGTAAAAA Intron 6 TAGgagaccagacgtagcggc
 catacaat0-----[1953035:1960-0>tacatctgccaatccatt
 gagtacgg gtcacgtgcatcgtagg

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Fig. 20 (continued)

```

gi|3599509|gb|A 269 TVMNEDRRGTYGLDCDWWSVGVVAYEMVYGKTPFTEGTSARTFNNIMNF
                    TVMN D +GTYGLDCDWWSVGV+AYEM+YG++PF EGTSARTFNNIMNF
                    TVMNGDGKGTYGLDCDWWSVGVIAAYEMIYGRSPFAEGTSARTFNNIMNF
gi|13653116|r1960491 agaagggagatgcgtgtttgggagtgaatgatctgggatgaataaaaaat
                    cttagagagcagtagaggctgttcaattaggcctcagcccgctaattat
                    tggcgtaaccccgctcggagcgtctggttgacctcagactcacctctgtc

gi|3599509|gb|A 318 Q                    RFLKFPDDPKVSSELLDLLQSLLCV
                    Q                    RFLKFPDDPKVSS+ LDL+QSLLC
                    Q                    RFLKFPDDPKVSSDFLDLIQSLLCG
gi|13653116|r1960638 cGTAAAGA Intron 7 CAGcttatcggcagaagtcgcacatttg
                    a0-----[1960641:1962-0>gttatcaacatggattattagttgg
                    g                    gtgatatccagctctttgtacggcc

gi|3599509|gb|A 344 QKERLKFEGLCCHPFFARTDWNINRN
                    QKERLKFEGLCCHPFF++ DWNINRN
                    QKERLKFEGLCCHPFFSKIDWNINRN S:S[tct]
gi|13653116|r1962909 cagacatggcttcctttaagtaaacaTGTAAGTA Intron 8
                    aaagtatagtggttcatagaatga 1-----[1962988:19824
                    gagaggtattccttcctatcgccttc

gi|3599509|gb|A 370 PPPFVPTLKSDDDTSNFDEPEKNSWAFILCVPAEPLAFSGEELP
                    PPPFVPTLKSDDDTSNFDEPEKNSW P FSGEELP
                    PPPFVPTLKSDDDTSNFDEPEKNSWSSSPCQLSPSGFSGEELP
gi|13653116|r1982415 CAGCTccctgcacatgggatatggcgaattgtttctccactgttgggcc
                    -1> cccttcctacaaaccataacaaacgtccccgatgccgtcgaatc
                    tcctccccgtctccctttaagggtggtactgcggccaccgtaagg

gi|3599509|gb|A 415 FVGFSYSKALGYLGRS SVVSSLD
                    FVGFSYSKALG LGRS SVVS LD
                    FVGFSYSKALGILGRS E:E[gag] SVVSGLD
gi|13653116|r1982552 tggtttaagcgacgatGAGTAAGTG Intron 9 TAGGtggtgcg
                    ttgtcagactgttggc 2-----[1982602:2000-2> cttcgta
                    tgggtgccgaggtttat ttggtgc

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Fig. 20 (continued)

```

gi|3599509|gb|A 439 SPAKVSSMEKKLLIKSKELQDSQDKCHK
                    SPAK SSMEKKLLIKSKELQDSQDKCHK
                    SPAKTSSMEKKLLIKSKELQDSQDKCHK
gi|13653116|r2000764 tcgaaatagaaccaaagccgctcgatcaGTATTTA Intron 10
                    cccacgctaaatttagaataacaaagaa0----- [2000848:20017
                    ctcgctccgagatccacagaactgcgctcg

gi|3599509|gb|A 467 MEQEMTRLHRRVSEVEAVLSQKEVELKASETQRSLLLEQDLATYITE
                    MEQEMTRLHRRVSEVEAVLSQKEVELKASETQRSLLLEQDLATYITE
                    MEQEMTRLHRRVSEVEAVLSQKEVELKASETQRSLLLEQDLATYITE
gi|13653116|r2001753 CAGagcgaactccagtgggggcacagggcagtgacatccgcgcgataag
                    -0>taaatcgtaggtcatacttgaaatataccacagcttaaatccatca
                    gggagcgatgagaggggtgttgggggggctgtgaccgggcttcccaa

gi|3599509|gb|A 513 CS SLKRSLEQARMEVSQEDDKALQLL
                    CS SLKRSLEQARMEVSQEDDKALQLL
                    CS SLKRSLEQARMEVSQEDDKALQLL
gi|13653116|r2001894 taGTGAGCC Intron 11 CAGatacatgcgcaggtcgggagcccc
                    gg0----- [2001900:2003-0>gtaggtaacgtatcaaaaactatt
                    ct cagatggaagggggcggtcaaggtc

gi|3599509|gb|A 539 HDIREQSRKLQEIQEYQAQVEEMR
                    HDIREQSRKLQEIQEYQAQVEEMR
                    HDIREQSRKLQEIQEYQAQVEEMR
gi|13653116|r2003242 cgaagcacaccgaagcGTAGGCC Intron 12 TAGgtcgcgggaa
                    aatgaaggataataaaa0----- [2003290:2008-0>aaacataatg
                    ttcaggcggaacagg gcgtagaagg

gi|3599509|gb|A 565 LMMNQLEEDLVSARRRSDLYESELRESRLAAEEFKRKANECQHKLK
                    LMMNQLEEDLVSARRRSDLYESELRESRLAAEEFKRKA ECQHKL+K
                    LMMNQLEEDLVSARRRSDLYESELRESRLAAEEFKRKATECQHKLK
gi|13653116|r2008995 taaactgggcgtgaacagctgtgcagtcgggggtacagagtccacta
                    tttataaattccggggataacatgacgtccaatagaccagaaatta
                    ggggtggagttcaaaagtccatggagtggtttaacggagaatgtaggg

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Fig. 20 (continued)

```

gi|3599509|gb|A 612      AKDQGKPEVGEYSKLEK
                        AKDQGKPEVGEY+KLEK
                        AKDQGKPEVGEYAKLEK
gi|13653116|r2009136 GTAGTCA Intron 13 CAGgagcgacggggtgacga
                        0-----[2009136:2009-0>caaagacatgaacataa
                        tgtaggtagaatgaggg

gi|3599509|gb|A 629      INAEQQLKIQELQEKLEK
                        INAEQQLKIQELQEKLEK
                        INAEQQLKIQELQEKLEK
gi|13653116|r2009450 GTATACT Intron 14 TAGaaggcccaacgccgacga
                        0-----[2009450:2009-0>tacaaatataataataa
                        cttgggcatggcagaggg

gi|3599509|gb|A 647      AVKASTEATELLQNIRQAKERAEREL
                        AVKASTEATELLQNIRQAKERAEREL
                        AVKASTEATELLQNIRQAKERAEREL
gi|13653116|r2010022 GTAAGCC Intron 15 TAGgggagaaggagcccaaccgagcggagc
                        0-----[2010022:2012-0>ctacgcaccattaatgacaagcagat
                        taaccggccggggtccgaggacgggg

gi|3599509|gb|A 673      EKLHNREDSSEGIKKLVEAE      ERRHS
                        EKL NREDSSEGI+KKLVEAE      ERRHS
                        EKLQNREDSSEGIKKLVEAE      ERRHS
gi|13653116|r2012975 gaccacggttgaaaaacggggGTGAGCA Intron 16 CAGgccct
                        aataagaaccagtgaattaca0-----[2013038:2014-0>aggac
                        ggggcagtttaccaggggatg      acctt

gi|3599509|gb|A 699      LENKVKRLETMERRENRLKDDIQTKSEQIQQMADKIL
                        LENKVKRLETMERRENRLKDDIQTKS+QIQQMADKIL
                        LENKVKRLETMERRENRLKDDIQTKSQIQQMADKIL
gi|13653116|r2014912 cgaagaacgaagcagaacaggacaatccaccaggaac
                        taaatagtactaggaagtaaatacacataatcaatt
                        ggcgagaagcggtaacagggtccgaacagcgggttatg

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Fig. 20 (continued)

```

gi|3599509|gb|A 736      ELEEKHREAQVSAQHLEVLKQKEQH
                        ELEEKHREAQVSAQHLEVLKQKEQH
                        ELEEKHREAQVSAQHLEVLKQKEQH
gi|13653116|r2015023 GTGAGCA Intron 17 TAGgcggaaccggcggtgcccgccacagcc
0-----[2015023:2018-0>ataaaagacatccaatatataaaaaa
                        gcagatggcacacgcaagcgagaggc

gi|3599509|gb|A 762 YEEKIK      VLDNQIKKDLADKESLENMM
                        YEEKIK      VLDNQIKKDLADKE+LENMM
                        YEEKIK      VLDNQIKKDLADKETLENMM
gi|13653116|r2018703 tggaaaGTAAAGA Intron 18 TAGgtgacaaagcggagacgaaa
aaaata0-----[2018721:2024-0>ttaaataaatcaaactaatt
tgagta      ggctgagacgtcggaggcgg

gi|3599509|gb|A 788 QRHEEEAHEKGKILSEQKA      MINAMDS
                        QRHEEEAHEKGKILSEQKA      MINAMDS
                        QRHEEEAHEKGKILSEQKA      MINAMDS
gi|13653116|r2024812 cacggggcgagaaacagcagGTAGGTA Intron 19 CAGaaagagt
agaaaacaaagattgaaac0-----[2024869:2027-0>ttactac
gacgggctggcatccagg      gcttgtc

gi|3599509|gb|A 814 KIRSLEQRIVELSEANKLAANSSLFTQRN
                        KIRSLEQRIVELSEANKLAANSSLFTQRN
                        KIRSLEQRIVELSEANKLAANSSLFTQRN
gi|13653116|r2027128 aaatcgcaaggctggaacggaaactacaa
atgctaagttatcaccaatccagggttcaga
gcacgaggtgagtactataatctttcagc

gi|3599509|gb|A 843      KAQEEMISELRQQKFYLETQAGK
                        KAQEEMISELRQQKFYLETQAGK
                        M:M[atg]      KAQEEMISELRQQKFYLETQAGK
gi|13653116|r2027215 ATGTAAGTA Intron 20 CAGGagcgggaatgcaccattcgacgga
2-----[2027217:2028-2>acaaattcatgaaatatacacga
                        gcaagggttacgagatcggagtgg

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Fig. 20 (continued)

gi|3599509|gb|A 867 LEAQNRLKEEQLEKISHQDHSDKSRLLELETRLRE
LEAQNRLKEEQLEKISHQDHSDK+RLLELETRLRE
LEAQNRLKEEQLEKISHQDHSDKNRLLELETRLRE

gi|13653116|r2028332 tggcacacggccgaaaccgcagaaccgcgaatcg
tacaagataaataatgaaaagaaagttatactga
ggcgcaagggggggccacctcgtgggaggaaggg

gi|3599509|gb|A 902 VSLEHEEQKLELKRQLTELQLSLQER
VSLEHEEQKLELKRQLTELQLSLQER
VSLEHEEQKLELKRQLTELQLSLQER

gi|13653116|r2028437 GTGAGAG Intron 21 CAGgacgcggcacgcacccagccctccgc
0-----[2028437:2033-0>tgtaaaaaatatagatcatatctaag
ctagcgggagggcgcgagagccgggc

gi|3599509|gb|A 928 ESQLTALQAARALESQLRQAKTELEETTAAEIEEEIQALT
ESQLTALQAARALESQLRQAKTELEETTAAEIEEEIQALT
ESQLTALQAARALESQLRQAKTELEETTAAEIEEEIQALT

gi|13653116|r2033637 gtctagccggcgggcagccccgaagcgggaaggggggacgca
acatcctaccgcctagatgacacataaccacaaaatactc
gaggacggtaggcggcgctcgggaggagcaaataggcgacg

gi|3599509|gb|A 968 AHRDEIQRKFDALRNSCT
AHRDEIQRKFDALRNSCT
AHRDEIQRKFDALRNSCT

gi|13653116|r2033757 GTAGGTC Intron 22 TAGgcaggaccatggccaata
0-----[2033757:2043-0>cagaatagatactgaggc
atatacgcatTTTTcctt

gi|3599509|gb|A 986 VITDLEEQLNQLTEDNAELNNQNFYL
VITDLEEQLNQLTEDNAELNNQNFYL
VITDLEEQLNQLTEDNAELNNQNFYL

gi|13653116|r2043396 GTGAGTA Intron 23 TAGgaagcggccaccaggaggcaacattt
0-----[2043396:2050-0>ttcataaataatcaaataaaaatat
acacgggggacggcgccctaccacccg

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Fig. 20 (continued)

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gi|3599509|gb|A 1012 SKQLDEASGANDEIVQLRSEVDHLRREITEREMQLTSQKQ
                      SKQLDEASGANDEIVQLRSEVDHLRREITEREMQLTSQKQ
                      SKQLDEASGANDEIVQLRSEVDHLRREITEREMQLTSQKQ
gi|13653116|r2050527 taccgggtggaggagcccagggccccgaagcgaccaaacac
                      caataaccgcaaattatggataatggatcagatatcgaaa
                      caactgttccccgtaagatagctccggcgaaggggtccgga

gi|3599509|gb|A 1052                      TMEALKTTCTMLEEQVLDLEALNDEL
                      TMEALKTTCTMLEEQV+DLEALNDEL
                      TMEALKTTCTMLEEQVMDLEALNDEL
gi|13653116|r2050647 GTAAGGA Intron 24 CAGaaggcaaataacggcgagtggcaggc
                      0-----[2050647:2051-0>ctactaccgcttaaattataactaaat
                      ggggtggcgccgggagcgtggcactgg

gi|3599509|gb|A 1078 LEKERQWEAWRSVLGDEKSQFECRVRELQRMLDTEKQS
                      LEKERQWEAWRSVLGDEKSQFECRVRELQRMLDTEKQS
                      LEKERQWEAWRSVLGDEKSQFECRVRELQRMLDTEKQS
gi|13653116|r2051527 cgagcctggtaagcgggatctgtcgcgccaacgagaca
                      taaagagacgggttgaaacataggtgatagttacaaag
                      aaagggggcgggccgttgacgtgtgtagggaggccgagc

gi|3599509|gb|A 1116                      ARADQRITESRQVVELAVKEHKA
                      ARADQRITESRQVVELAVKEHKA
                      R:R[agg] ARADQRITESRQVVELAVKEHKA
gi|13653116|r2051641 AGGTGGGGC Intron 25 CAGGgaggccaagtccgggaggagcag
                      2-----[2051643:2055-2>cgcaagtcacgattatctaaaac
                      gactggccgctcgggggagggcgct

gi|3599509|gb|A 1140 EILALQQALKEQKLKAESLSDK                      LNDL
                      EILALQQALKEQKLKAESLSDK                      LNDL
                      EILALQQALKEQKLKAESLSDK                      LNDL
gi|13653116|r2055246 gacgcccgcagcacaggactgaGTCAGCG Intron 26 TAGcagc
                      attctaactaaaaatacagtaa0-----[2055312:2057-0>taat
                      gtctgggtcagggggcgccctcg                      ctcg

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Fig. 20 (continued)

gi|3599509|gb|A 1166 EKKHAMLEMNARSLQQKLETERELKQRLLEE
EKKHAMLEMNARSLQQKLETERELKQRLLEE
EKKHAMLEMNARSLQQKLETERELKQRLLEE
gi|13653116|r2057212 gaacgacgaagcatccacgagcgacaccgg
aaaacttatacggtaaatacagataagttaa
gggttgtagtcacagggggtaagcaggtgag

gi|3599509|gb|A 1197 QAKLQQQMDLQKNHIFRLTQGLQEAL
QAKLQQQMDLQKNHIFRLTQGLQEAL
QAKLQQQMDLQKNHIFRLTQGLQEAL
gi|13653116|r2057305 GTGAGTG Intron 27 TAGcgatcccagccaacatccacgccggc
0-----[2057305:2064-0>acataaatataaaaattgtcagtaact
acaagggggcggatctctgtaagaata

gi|3599509|gb|A 1223 DRADLLKTERS DLEYQLENIQ VLYSH
DRADLLKTERS DLEYQLENIQ VLYSH
DRADLLKTERS DLEYQLENIQ VLYSH
gi|13653116|r2064435 gcggccaagaagtgtccgaacGTGAGGA Intron 28 TAGgcttc
agcattacaggataaataa0-----[2064498:2065-0>ttaca
tgtaggaaatcgggtggactg tcttt

gi|3599509|gb|A 1249 EKVKMEGTISQQTKLIDFLQAKMDQPAK KKK
EKVKMEGTISQQTKLIDFLQAKMDQPAK KKK
EKVKMEGTISQQTKLIDFLQAKMDQPAK KKK
gi|13653116|r2065236 gagaaggaatccaacagtccgaagccgaaaa
aatatagctcaacattattacataacccaaaa
aggagactttaacactttgacagcattagag

gi|3599509|gb|A 1280 VPLQYNELKLALALEKEKARCAELEEEAL
VPLQYNELKLALALEKEKARCAELEEEAL
VPLQYNELKLALALEKEKARCAELEEEAL
gi|13653116|r2065329 GTGAGTC Intron 29 CAGgccctagcacgcgagagctggcggggc
0-----[2065329:2066-0>tctaaaatatctaaaacggcataact
ttggctggggcggggatctagagact

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Fig. 20 (continued)

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gi|3599509|gb|A 1306 QKTRIELRSAREE                AHRKATDHPH
                    QKTRIELRSAREE                AHRKATDHPH
                    QKTRIELRSAREE                A:A[gct]    AHRKATDHPH
gi|13653116|r2067068 caacagcctgcgggGGTAGGGG Intron 30 CAGCTgccagagccc
                    aacgtatgccgaa 1-----[2067108:2067-1> cagaccaaca
                    ggccccgcgccgga                cccaagccac

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gi|3599509|gb|A 1330 PSTPATARQQIAMSIAIVRSPEHQPSAMSLAPPSSRRKESSTPE
                    PSTPATARQQIAMSIAIVRSPEHQPSAMSLAPPSSRRKESSTPE
                    PSTPATARQQIAMSIAIVRSPEHQPSAMSLAPPSSRRKESSTPE
gi|13653116|r2067429 ctacgagaccagatgagctcgcccagaaccgcctacaagttacg
                    cccccccgaatctccttgccaaacgctgttccccgggaacccca
                    acgaccggggcccgccgggagcgctcgcgcgaccagggtatag

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gi|3599509|gb|A 1374                FSRRLKERMHHNIPHRFNVGLNM
                    FSRRLKERMHHNIPHRFNVGLNM
                    E:E[gaa]          FSRRLKERMHHNIPHRFNVGLNM
gi|13653116|r2067561 GGTACGTT Intron 31 CAGAAatcccagcaccaaccctaggcaa
                    1-----[2067562:2071-1> tgggtaagtaaatacgtatgtat
                    ttgttgacgcctttcaccaagcg

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```

gi|3599509|gb|A 1398 RATKCAVCLDTVHFGRQASKCL                C
                    RATKCAVCLDTVHFGRQASKCL                C
                    RATKCAVCLDTVHFGRQASKCL                E:E[gaa]    C
gi|13653116|r2071543 cgaatggtcgagctgccgtatcGGTAAGAT Intron 32 TAGAAt
                    gccagctgtactatggaccagt 1-----[2071610:2072-1> g
                    acagttgtgtcgctacgacatc                t

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```

gi|3599509|gb|A 1422 QVMCHPKCSTCLPATCGLPAEYATHFTEAFCDKMNSPGLQSKPEGSSSL
                    QVMCHPKCSTCLPATCGLPAEYATHFTEAFCDKMNSPGLQ+KEP SSL
                    QVMCHPKCSTCLPATCGLPAEYATHFTEAFCDKMNSPGLQTKPESSSL
gi|13653116|r2072163 cgatccattattcgatgtcggtgactaggttcgaaatcgccaagcaaat
                    attgacagccgtcccgggtccaaccatcactggaataccgtacaacgggt
                    ggggtccgcgcgcgacccccgttatcacccgccctcagccatcgcgggccccg

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Fig. 20 (continued)

```

gi|3599509|gb|A 1471 HLEGWMKVP                      NNKRGGQQGWDRKYI
                     HLEGWMKVP                      NNKRGGQQGWDRKYI
                     HLEGWMKVP                      R:R[agg] NNKRGGQQGWDRKYI
gi|13653116|r2072310 ccggtaaagcAGGTACCAT Intron 33 CAGGaaacgccgtgaata
                     ataggtatc 2-----[2072339:2072-2> aaaggaaggagaat
                     cgaggggggc                      tcaaagacgcggct

```

```

gi|3599509|gb|A 1495 VLEGSKVLIYDNEARE                GQRPVEE
                     VLEGSKVLIYDNEARE                GQRPVEE
                     VLEGSKVLIYDNEARE                A:A[gct] GQRPVEE
gi|13653116|r2072555 gcggtagcatgaggagGGTAAATT Intron 34 AAGCTgcacggg
                     ttagcatttaaaacga 1-----[2072604:2073-1> gagctaa
                     cggaaccttctacaa                  aggggaa

```

```

gi|3599509|gb|A 1519 FELCLPDGDVSIHGAVGASELANTAKA
                     FELCLPDGDVSIHGAVGASELANTAKA
                     FELCLPDGDVSIHGAVGASELANTAKA    D:D[gat]
gi|13653116|r2073134 tgctccgggggtacgggggtgcgaagagGGTGAGGA Intron 35
                     tatgtcagatctagctgccatcaccac 1-----[2073216:20734
                     tggctccgtattttctttcacatacaa

```

```

gi|3599509|gb|A 1546 VPYILKMESHPTTCWPGRTLyllapsfPDKQRWVTALESVVAG
                     VPYILKMESHPTTCWPGRTLyllapsfPDKQRWVTALESVVAG
                     VPYILKMESHPTTCWPGRTLyllapsfPDKQRWVTALESVVAG
gi|13653116|r2073456 TAGATgctacaagtccaattcgaacttcgcacacgacctgagtgtgggg
                     -1> tcattatacacaccggcggtattccgtcaaaggctcctacttcg
                     cacagggatcgccccgcgacccgatccctcagcgcccaaatcat

```

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gi|3599509|gb|A 1591 GRVSREKAEADA                    KLLGNSLLKLEGDD
                     GRVSREKAEADA                    KLLGNSLLKLEGDD
                     GRVSREKAEADA                    KLLGNSLLKLEGDD
gi|13653116|r2073593 gagtagagggggGTGAGTA Intron 36 AAGaccgatccacgggg
                     ggtcgaacacac0-----[2073629:2075-0>attgacttatagaa
                     gattgaaaattt                    agtaccggagattc

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Fig. 20 (continued)

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gi|3599509|gb|A 1617 RLD MNCTLPFSDQ VVLVGTEEGLYAL
                      RLD MNCTLPFSDQ VVLVGTEEGLYAL
                      RLD MNCTLPFSDQ VVLVGTEEGLYAL
gi|13653116|r2075228 ccgaatacctagcGTAATGC Intron 37 CAGggtggagggctgc
                      gtatagctctgaa0-----[2075267:2075-0>ttttgcaagtact
                      tacgccggcctcg ggggccgagcccg

gi|3599509|gb|A 1643 NVLKNLSLTHIPGIGAVFQIYIIKDLEKLLMIA
                      NVLKNLSLTH+PGIGAVFQIYIIKDLEKLLMIA
                      NVLKNLSLTHVPGIGAVFQIYIIKDLEKLLMIA
gi|13653116|r2075459 agtaatcacgcgaggggtcataaagcgaccaag
                      attaactcatcgtgcttatattaataattttc
                      tcgaccactcaataaccattttcgcgggacgaa

gi|3599509|gb|A 1675 EERALCLVDVKKVKQSLAQSHLP
                      EERALCLVDVKKVKQSLAQSHLP
                      G:G[gga] EERALCLVDVKKVKQSLAQSHLP
gi|13653116|r2075555 GGTGTGAG Intron 38 CAGGAggcgctcggaagactcgctccc
                      1-----[2075556:2077-1> aagctgttataataactcacatc
                      aggagttgcggagagcgcgccgt

gi|3599509|gb|A 1699 AQP DVSPNIFEAVKGCHLFAAGK IEN
                      AQP D+SPNIFEAVKGCHLF AGK IEN
                      AQP DISPNIFEAVKGCHLFGAGK IEN
gi|13653116|r2077559 gccgatcaatgggagtccttggaGTAAGCT Intron 39 CAGaga
                      cacatccattactaggattgcga0-----[2077628:2081-0>taa
                      cgcccaccttatcgcccgtagcg tgc

gi|3599509|gb|A 1725 SLCICAAMPSKVILRYNDNLSKYCIRK
                      LCICAAMPSKVILRYN+NLSKYCIRK
                      GLCICAAMPSKVILRYNENLSKYCIRK
gi|13653116|r2081360 gctatggacaaggacctagacaattacaGTAAGTC Intron 40
                      gtgtgcctcgattttgaaaatgaagtga0-----[2081444:20838
                      gccctacgccacctccccacccaccga

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Fig. 20 (continued)

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gi|3599509|gb|A 1753      EIETSEPCSCIHFTNYSILIGTNKFYEIDMKQYTL
                        EIETSEPCSCIHFTNYSILIGTNKFYEIDMKQYTL+
                        EIETSEPCSCIHFTNYSILIGTNKFYEIDMKQYTL
gi|13653116|r2083845 CAGgagatgctataactaataacagaaattgagaactacg
                        -0>ataccacgggtatcaagtttgcaataatataaacta
                        gagcagccctcccctctcctactaccaccggggcgcg

gi|3599509|gb|A 1789      FLDKNDHSLAPAVFASSNSFPV
                        FLDKNDHSLAPAVFA+SSNSFPV
                        E:E[gaa]      FLDKNDHSLAPAVFAASSNSFPV
gi|13653116|r2083956 GGTAGGAC Intron 41 CAGAAtcgaagcttgcggtggttaatcg
                        1-----[2083957:2084-1> ttaaaaactcccttccccagtct
                        cgtgtctcgattgtcctccctc

gi|3599509|gb|A 1813 SIVQANSAGQREEYLLCFH      FGVF
                        SIVQ NSAGQREEYLLCFH      FGVF
                        SIVQVNSAGQREEYLLCFH      E:E[gaa]      FGVF
gi|13653116|r2084125 tagcgaaggccggttcttcGGTGAGTC Intron 42 CAGAAtggt
                        cttatagcgagaaattgta 1-----[2084183:2084-1> tggt
                        acggggccaggaggcggtcc      tagc

gi|3599509|gb|A 1837 VDSYGRRSRTDDLKWSRLPLAF      Y
                        VDSYGRRSRTDDLKWSRLPLAF      Y
                        VDSYGRRSRTDDLKWSRLPLAF      A:A[gcc]      Y
gi|13653116|r2084995 ggttgacacaggcatactctgtGGTACGTG Intron 43 CAGCct
                        tacaggggggcaatagggctctct 1-----[2085062:2087-1> a
                        gttcaatccactcgggtcatgct      c

gi|3599509|gb|A 1861 REPYLEFVTHFNSLEVIEIQARSSL
                        REPYLEFVTHFNSLEVIEIQARSS
                        REPYLEFVTHFNSLEVIEIQARSSA      G:G[ggg]
gi|13653116|r2087757 agctctgactatcggagacgcttgGGGTAAGCA Intron 44
                        gacatttcatactattatacgccc 2-----[2087831:20879
                        aactgtgccccacaaatgcgaccaa

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Fig. 20 (continued)

gi|3599509|gb|A 1885 SPARAYLEIPNPRYLGPATSSGAIYLASSYQDKLRVICCKGNLVK
+PARAYL+IPNPRYLGPATSSGAIYLASSYQDKLRVICCKGNLVK
TPARAYLDIPNPRYLGPATSSGAIYLASSYQDKLRVICCKGNLVK
gi|13653116|r2087965 CAGGacgcgctcgacacctcgcgattggattgtttcgatagattagacga
-2> cccgcatatcacgatgcctccgctatcccaaatgttggagatta
ctcagcgccgcgcgctctcaagtcggcacgtaagctccgaccgg

gi|3599509|gb|A 1931 ESGTEQHRVPSTSR SPNKRGPPT
ESGTE HR PSTSR SPNKRGPPT
ESGTEHHRGPSTSR S:S[agc] SPNKRGPPT
gi|13653116|r2088104 gtgagcccgcctatcAGGTAACCA Intron 45 CAGCacaacgccca
acgcaaaggccccc 2-----[2088148:2095-2> gcaaggccc
gcctaccgcgcccc cccgacacg

gi|3599509|gb|A 1955 YNEHITKRVASSPAPPEGPSHPREPSTPHRYRDREGTELRRDKSPGRP
YNEHITKRVASSPAPPEGPSHPREPSTPHRYR EGTELRRDKSPGRP
YNEHITKRVASSPAPPEGPSHPREPSTPHRYR--EGTELRRDKSPGRP
gi|13653116|r2095380 tagcaaacggtacgccggcaccgcgaaccctc ggcagccagatcgcc
aaaatcagtcgccccagcgacgacgccagag aggcattggaaccggc
ccgcccgcgcccaggcaccgcgagacaccccc gggcggcgcggtccc

gi|3599509|gb|A 2004 LEREKSPGRMLSTRRERSPGRLFEDSSRGRLPAGAVRTPLSQVNKVDQ
LEREKSPGRMLSTRRERSPGRLFEDSSRGRLPAGAVRTPLSQVNKV
LEREKSPGRMLSTRRERSPGRLFEDSSRGRLPAGAVRTPLSQVNKVRQH
gi|13653116|r2095521 cgcgatcgacaaacagctcgactggaaagcccggggaacctcgaagacc
tagaaccggttgcggagccggttaaggggtccgctgcctcataatgaa
ggaggcccgccggaggccgggtacccgcggtgacggcgccggcggtt

gi|3599509|gb|A 2053 S
S
S
gi|13653116|r2095668 t
c
c

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Fig. 20 (continued)

gi 13653116 ref NT_009775.3 Hs12_9932	GeneWise	match	1909637	2095670
3906.49				
+ . gi 3599509 gb AAC72823.1				
gi 13653116 ref NT_009775.3 Hs12_9932	GeneWise	cds	1909637	1909732
0.00				
+ 0 gi 3599509 gb AAC72823.1				
gi 13653116 ref NT_009775.3 Hs12_9932	GeneWise	intron	1909733	1916603
0.00				
+ . gi 3599509 gb AAC72823.1				
gi 13653116 ref NT_009775.3 Hs12_9932	GeneWise	cds	1916604	1916745
0.00				
+ 0 gi 3599509 gb AAC72823.1				
gi 13653116 ref NT_009775.3 Hs12_9932	GeneWise	intron	1916746	1928106
0.00				
+ . gi 3599509 gb AAC72823.1				
gi 13653116 ref NT_009775.3 Hs12_9932	GeneWise	cds	1928107	1928282
0.00				
+ 2 gi 3599509 gb AAC72823.1				
gi 13653116 ref NT_009775.3 Hs12_9932	GeneWise	intron	1928283	1935529
0.00				
+ . gi 3599509 gb AAC72823.1				
gi 13653116 ref NT_009775.3 Hs12_9932	GeneWise	cds	1935530	1935631
0.00				
+ 0 gi 3599509 gb AAC72823.1				
gi 13653116 ref NT_009775.3 Hs12_9932	GeneWise	intron	1935632	1951576
0.00				
+ . gi 3599509 gb AAC72823.1				
gi 13653116 ref NT_009775.3 Hs12_9932	GeneWise	cds	1951577	1951719
0.00				
+ 0 gi 3599509 gb AAC72823.1				
gi 13653116 ref NT_009775.3 Hs12_9932	GeneWise	intron	1951720	1952940
0.00				
+ . gi 3599509 gb AAC72823.1				
gi 13653116 ref NT_009775.3 Hs12_9932	GeneWise	cds	1952941	1953034
0.00				
+ 1 gi 3599509 gb AAC72823.1				
gi 13653116 ref NT_009775.3 Hs12_9932	GeneWise	intron	1953035	1960436
0.00				
+ . gi 3599509 gb AAC72823.1				

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Fig. 20 (continued)

gi 13653116 ref NT_009775.3 Hs12_9932	GeneWise	cds	1960437	1960640
0.00				
+ 0 gi 3599509 gb AAC72823.1				
gi 13653116 ref NT_009775.3 Hs12_9932	GeneWise	intron	1960641	1962833
0.00				
+ . gi 3599509 gb AAC72823.1				
gi 13653116 ref NT_009775.3 Hs12_9932	GeneWise	cds	1962834	1962987
0.00				
+ 0 gi 3599509 gb AAC72823.1				
gi 13653116 ref NT_009775.3 Hs12_9932	GeneWise	intron	1962988	1982417
0.00				
+ . gi 3599509 gb AAC72823.1				
gi 13653116 ref NT_009775.3 Hs12_9932	GeneWise	cds	1982418	1982601
0.00				
+ 2 gi 3599509 gb AAC72823.1				
gi 13653116 ref NT_009775.3 Hs12_9932	GeneWise	intron	1982602	2000741
0.00				
+ . gi 3599509 gb AAC72823.1				
gi 13653116 ref NT_009775.3 Hs12_9932	GeneWise	cds	2000742	2000847
0.00				
+ 1 gi 3599509 gb AAC72823.1				
gi 13653116 ref NT_009775.3 Hs12_9932	GeneWise	intron	2000848	2001755
0.00				
+ . gi 3599509 gb AAC72823.1				
gi 13653116 ref NT_009775.3 Hs12_9932	GeneWise	cds	2001756	2001899
0.00				
+ 0 gi 3599509 gb AAC72823.1				
gi 13653116 ref NT_009775.3 Hs12_9932	GeneWise	intron	2001900	2003169
0.00				
+ . gi 3599509 gb AAC72823.1				
gi 13653116 ref NT_009775.3 Hs12_9932	GeneWise	cds	2003170	2003289
0.00				
+ 0 gi 3599509 gb AAC72823.1				
gi 13653116 ref NT_009775.3 Hs12_9932	GeneWise	intron	2003290	2008964
0.00				
+ . gi 3599509 gb AAC72823.1				

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Fig. 20 (continued)

gi 13653116 ref NT_009775.3 Hs12_9932	GeneWise	cds	2008965	2009135
0.00				
+ 0 gi 3599509 gb AAC72823.1				
gi 13653116 ref NT_009775.3 Hs12_9932	GeneWise	intron	2009136	2009398
0.00				
+ . gi 3599509 gb AAC72823.1				
gi 13653116 ref NT_009775.3 Hs12_9932	GeneWise	cds	2009399	2009449
0.00				
+ 0 gi 3599509 gb AAC72823.1				
gi 13653116 ref NT_009775.3 Hs12_9932	GeneWise	intron	2009450	2009967
0.00				
+ . gi 3599509 gb AAC72823.1				
gi 13653116 ref NT_009775.3 Hs12_9932	GeneWise	cds	2009968	2010021
0.00				
+ 0 gi 3599509 gb AAC72823.1				
gi 13653116 ref NT_009775.3 Hs12_9932	GeneWise	intron	2010022	2012896
0.00				
+ . gi 3599509 gb AAC72823.1				
gi 13653116 ref NT_009775.3 Hs12_9932	GeneWise	cds	2012897	2013037
0.00				
+ 0 gi 3599509 gb AAC72823.1				
gi 13653116 ref NT_009775.3 Hs12_9932	GeneWise	intron	2013038	2014896
0.00				
+ . gi 3599509 gb AAC72823.1				
gi 13653116 ref NT_009775.3 Hs12_9932	GeneWise	cds	2014897	2015022
0.00				
+ 0 gi 3599509 gb AAC72823.1				
gi 13653116 ref NT_009775.3 Hs12_9932	GeneWise	intron	2015023	2018624
0.00				
+ . gi 3599509 gb AAC72823.1				
gi 13653116 ref NT_009775.3 Hs12_9932	GeneWise	cds	2018625	2018720
0.00				
+ 0 gi 3599509 gb AAC72823.1				
gi 13653116 ref NT_009775.3 Hs12_9932	GeneWise	intron	2018721	2024751
0.00				
+ . gi 3599509 gb AAC72823.1				

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Fig. 20 (continued)

gi 13653116 ref NT_009775.3 Hs12_9932	GeneWise	cds	2024752	2024868
0.00				
+ 0 gi 3599509 gb AAC72823.1				
gi 13653116 ref NT_009775.3 Hs12_9932	GeneWise	intron	2024869	2027106
0.00				
+ . gi 3599509 gb AAC72823.1				
gi 13653116 ref NT_009775.3 Hs12_9932	GeneWise	cds	2027107	2027216
0.00				
+ 0 gi 3599509 gb AAC72823.1				
gi 13653116 ref NT_009775.3 Hs12_9932	GeneWise	intron	2027217	2028261
0.00				
+ . gi 3599509 gb AAC72823.1				
gi 13653116 ref NT_009775.3 Hs12_9932	GeneWise	cds	2028262	2028436
0.00				
+ 1 gi 3599509 gb AAC72823.1				
gi 13653116 ref NT_009775.3 Hs12_9932	GeneWise	intron	2028437	2033558
0.00				
+ . gi 3599509 gb AAC72823.1				
gi 13653116 ref NT_009775.3 Hs12_9932	GeneWise	cds	2033559	2033756
0.00				
+ 0 gi 3599509 gb AAC72823.1				
gi 13653116 ref NT_009775.3 Hs12_9932	GeneWise	intron	2033757	2043341
0.00				
+ . gi 3599509 gb AAC72823.1				
gi 13653116 ref NT_009775.3 Hs12_9932	GeneWise	cds	2043342	2043395
0.00				
+ 0 gi 3599509 gb AAC72823.1				
gi 13653116 ref NT_009775.3 Hs12_9932	GeneWise	intron	2043396	2050448
0.00				
+ . gi 3599509 gb AAC72823.1				
gi 13653116 ref NT_009775.3 Hs12_9932	GeneWise	cds	2050449	2050646
0.00				
+ 0 gi 3599509 gb AAC72823.1				
gi 13653116 ref NT_009775.3 Hs12_9932	GeneWise	intron	2050647	2051448
0.00				
+ . gi 3599509 gb AAC72823.1				

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Fig. 20 (continued)

gi 13653116 ref NT_009775.3 Hs12_9932	GeneWise	cds	2051449	2051642
0.00				
+ 0 gi 3599509 gb AAC72823.1				
gi 13653116 ref NT_009775.3 Hs12_9932	GeneWise	intron	2051643	2055175
0.00				
+ . gi 3599509 gb AAC72823.1				
gi 13653116 ref NT_009775.3 Hs12_9932	GeneWise	cds	2055176	2055311
0.00				
+ 1 gi 3599509 gb AAC72823.1				
gi 13653116 ref NT_009775.3 Hs12_9932	GeneWise	intron	2055312	2057199
0.00				
+ . gi 3599509 gb AAC72823.1				
gi 13653116 ref NT_009775.3 Hs12_9932	GeneWise	cds	2057200	2057304
0.00				
+ 0 gi 3599509 gb AAC72823.1				
gi 13653116 ref NT_009775.3 Hs12_9932	GeneWise	intron	2057305	2064356
0.00				
+ . gi 3599509 gb AAC72823.1				
gi 13653116 ref NT_009775.3 Hs12_9932	GeneWise	cds	2064357	2064497
0.00				
+ 0 gi 3599509 gb AAC72823.1				
gi 13653116 ref NT_009775.3 Hs12_9932	GeneWise	intron	2064498	2065220
0.00				
+ . gi 3599509 gb AAC72823.1				
gi 13653116 ref NT_009775.3 Hs12_9932	GeneWise	cds	2065221	2065328
0.00				
+ 0 gi 3599509 gb AAC72823.1				
gi 13653116 ref NT_009775.3 Hs12_9932	GeneWise	intron	2065329	2066989
0.00				
+ . gi 3599509 gb AAC72823.1				
gi 13653116 ref NT_009775.3 Hs12_9932	GeneWise	cds	2066990	2067107
0.00				
+ 0 gi 3599509 gb AAC72823.1				
gi 13653116 ref NT_009775.3 Hs12_9932	GeneWise	intron	2067108	2067396
0.00				
+ . gi 3599509 gb AAC72823.1				

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Fig. 20 (continued)

gi 13653116 ref NT_009775.3 Hs12_9932	GeneWise	cds	2067397	2067561
0.00				
+ 2 gi 3599509 gb AAC72823.1				
gi 13653116 ref NT_009775.3 Hs12_9932	GeneWise	intron	2067562	2071471
0.00				
+ . gi 3599509 gb AAC72823.1				
gi 13653116 ref NT_009775.3 Hs12_9932	GeneWise	cds	2071472	2071609
0.00				
+ 2 gi 3599509 gb AAC72823.1				
gi 13653116 ref NT_009775.3 Hs12_9932	GeneWise	intron	2071610	2072157
0.00				
+ . gi 3599509 gb AAC72823.1				
gi 13653116 ref NT_009775.3 Hs12_9932	GeneWise	cds	2072158	2072338
0.00				
+ 2 gi 3599509 gb AAC72823.1				
gi 13653116 ref NT_009775.3 Hs12_9932	GeneWise	intron	2072339	2072511
0.00				
+ . gi 3599509 gb AAC72823.1				
gi 13653116 ref NT_009775.3 Hs12_9932	GeneWise	cds	2072512	2072603
0.00				
+ 1 gi 3599509 gb AAC72823.1				
gi 13653116 ref NT_009775.3 Hs12_9932	GeneWise	intron	2072604	2073110
0.00				
+ . gi 3599509 gb AAC72823.1				
gi 13653116 ref NT_009775.3 Hs12_9932	GeneWise	cds	2073111	2073215
0.00				
+ 2 gi 3599509 gb AAC72823.1				
gi 13653116 ref NT_009775.3 Hs12_9932	GeneWise	intron	2073216	2073458
0.00				
+ . gi 3599509 gb AAC72823.1				
gi 13653116 ref NT_009775.3 Hs12_9932	GeneWise	cds	2073459	2073628
0.00				
+ 2 gi 3599509 gb AAC72823.1				
gi 13653116 ref NT_009775.3 Hs12_9932	GeneWise	intron	2073629	2075185
0.00				
+ . gi 3599509 gb AAC72823.1				

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Fig. 20 (continued)

gi 13653116 ref NT_009775.3 Hs12_9932	GeneWise	cds	2075186	2075266
0.00				
+ 0 gi 3599509 gb AAC72823.1				
gi 13653116 ref NT_009775.3 Hs12_9932	GeneWise	intron	2075267	2075419
0.00				
+ . gi 3599509 gb AAC72823.1				
gi 13653116 ref NT_009775.3 Hs12_9932	GeneWise	cds	2075420	2075555
0.00				
+ 0 gi 3599509 gb AAC72823.1				
gi 13653116 ref NT_009775.3 Hs12_9932	GeneWise	intron	2075556	2077487
0.00				
+ . gi 3599509 gb AAC72823.1				
gi 13653116 ref NT_009775.3 Hs12_9932	GeneWise	cds	2077488	2077627
0.00				
+ 2 gi 3599509 gb AAC72823.1				
gi 13653116 ref NT_009775.3 Hs12_9932	GeneWise	intron	2077628	2081350
0.00				
+ . gi 3599509 gb AAC72823.1				
gi 13653116 ref NT_009775.3 Hs12_9932	GeneWise	cds	2081351	2081443
0.00				
+ 0 gi 3599509 gb AAC72823.1				
gi 13653116 ref NT_009775.3 Hs12_9932	GeneWise	intron	2081444	2083847
0.00				
+ . gi 3599509 gb AAC72823.1				
gi 13653116 ref NT_009775.3 Hs12_9932	GeneWise	cds	2083848	2083956
0.00				
+ 0 gi 3599509 gb AAC72823.1				
gi 13653116 ref NT_009775.3 Hs12_9932	GeneWise	intron	2083957	2084053
0.00				
+ . gi 3599509 gb AAC72823.1				
gi 13653116 ref NT_009775.3 Hs12_9932	GeneWise	cds	2084054	2084182
0.00				
+ 2 gi 3599509 gb AAC72823.1				
gi 13653116 ref NT_009775.3 Hs12_9932	GeneWise	intron	2084183	2084980
0.00				
+ . gi 3599509 gb AAC72823.1				

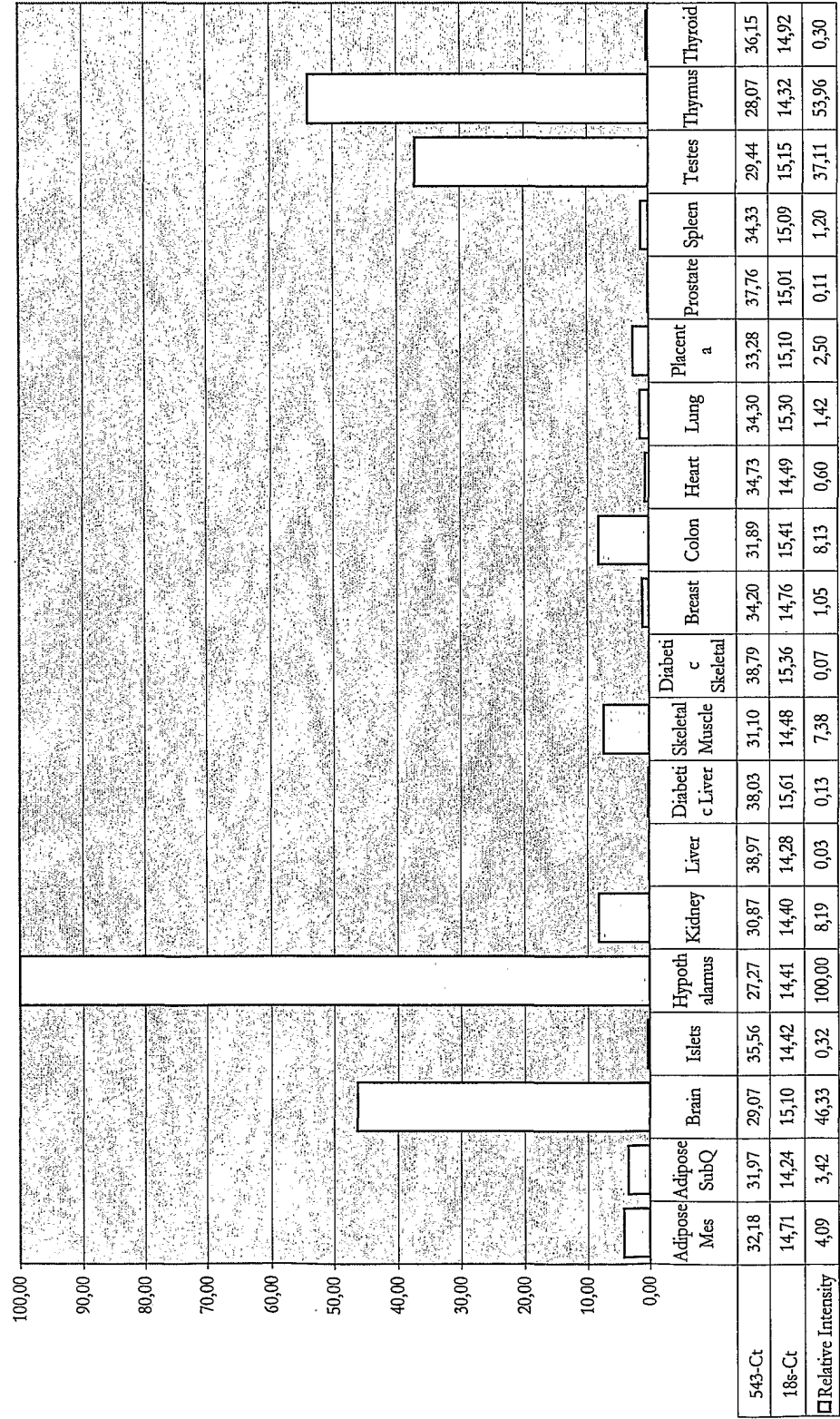
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Fig. 20 (continued)

gi 13653116 ref NT_009775.3 Hs12_9932	GeneWise	cds	2084981	2085061
0.00				
+ 2 gi 3599509 gb AAC72823.1				
gi 13653116 ref NT_009775.3 Hs12_9932	GeneWise	intron	2085062	2087751
0.00				
+ . gi 3599509 gb AAC72823.1				
gi 13653116 ref NT_009775.3 Hs12_9932	GeneWise	cds	2087752	2087830
0.00				
+ 2 gi 3599509 gb AAC72823.1				
gi 13653116 ref NT_009775.3 Hs12_9932	GeneWise	intron	2087831	2087967
0.00				
+ . gi 3599509 gb AAC72823.1				
gi 13653116 ref NT_009775.3 Hs12_9932	GeneWise	cds	2087968	2088147
0.00				
+ 1 gi 3599509 gb AAC72823.1				
gi 13653116 ref NT_009775.3 Hs12_9932	GeneWise	intron	2088148	2095351
0.00				
+ . gi 3599509 gb AAC72823.1				
gi 13653116 ref NT_009775.3 Hs12_9932	GeneWise	cds	2095352	2095670
0.00				
+ 1 gi 3599509 gb AAC72823.1				

FIG. 21

LBRI 543: Relative Expression



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Fig. 22

TBLASTN - alignment of 543_Protein against emnew|AX166510|AX166510
Sequence 1 from Patent WO0138503.//:gbnew|AX166510|AX166510 Sequence 1 from
Patent WO0138503.

This hit is scoring at : 0.0 (expectation value)
Alignment length (overlap) : 2053
Identities : 99 %
Scoring matrix : BLOSUM62 (used to infer consensus pattern)
Hit reading frame : +1
Database searched : nrnee_1_;

Q: 1 MLKFKYGARNPLDAGAAEPIASRASRLNLFFQGKPPFMTQQQMSPLSREGILDALFVLFE
MLKFKYGARNPLDAGAAEPIASRASRLNLFFQGKPPFMTQQQMSPLSREGILDALFVLFE
H: 1 MLKFKYGARNPLDAGAAEPIASRASRLNLFFQGKPPFMTQQQMSPLSREGILDALFVLFE

ECSQPALMKIKHVSNFVRK-YSDTIAELQELQPSAKDFEVRSLVGCGHFAEVQVVREKAT
ECSQPALMKIKHVSNFV : YSDTIAELQELQPSAKDFEVRSLVGCGHFAEVQVVREKAT
ECSQPALMKIKHVSNFVPEVYSDTIAELQELQPSAKDFEVRSLVGCGHFAEVQVVREKAT

GDIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLYLVMEYQPG
GDIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLYLVMEYQPG
GDIYAMKVMKKKALLAQEQVSFFEEERNILSRSTSPWIPQLQYAFQDKNHLYLVMEYQPG

GDLLSLLNRYEDQLDENLIQFYLAELILAVHSVHLMGYVHRDIKPENILVDRTGHIKLVD
GDLLSLLNRYEDQLDENLIQFYLAELILAVHSVHLMGYVHRDIKPENILVDRTGHIKLVD
GDLLSLLNRYEDQLDENLIQFYLAELILAVHSVHLMGYVHRDIKPENILVDRTGHIKLVD

FGSAKMNSNKMVNAKLPIGTPDYMAPEVLTVMNGDGKGTYGLDCDWWSVGVIAYEMIYG
FGSAKMNSNKMVNAKLPIGTPDYMAPEVLTVMNGDGKGTYGLDCDWWSVGVIAYEMIYG
FGSAKMNSNKMVNAKLPIGTPDYMAPEVLTVMNGDGKGTYGLDCDWWSVGVIAYEMIYG

RSPFAEGTSARTFNNIMNFQRFKFPDDPKVSSDFLDLIQSLLCGQKERLKFEGLCCHPF
RSPFAEGTSARTFNNIMNFQRFKFPDDPKVSSDFLDLIQSLLCGQKERLKFEGLCCHPF
RSPFAEGTSARTFNNIMNFQRFKFPDDPKVSSDFLDLIQSLLCGQKERLKFEGLCCHPF

FSKIDWNNIRNSPPPFVPTLKSDDDTSNFDEPEKNSWVSSSPCQLSPSGFSGEELPFVGF
FSKIDWNNIRNSPPPFVPTLKSDDDTSNFDEPEKNSWVSSSPCQLSPSGFSGEELPFVGF
FSKIDWNNIRNSPPPFVPTLKSDDDTSNFDEPEKNSWVSSSPCQLSPSGFSGEELPFVGF

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Fig. 22 (continued)

SYSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKMEQEMTRLHRRV
SYSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKMEQEMTRLHRRV
SYSKALGILGRSESVVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHKMEQEMTRLHRRV

SEVEAVLSQKEVELKASETQRSLLLEQDLATYITECSSLKRSLEQARMEVSQEDDKALQLL
SEVEAVLSQKEVELKASETQRSLLLEQDLATYITECSSLKRSLEQARMEVSQEDDKALQLL
SEVEAVLSQKEVELKASETQRSLLLEQDLATYITECSSLKRSLEQARMEVSQEDDKALQLL

HDIREQSRKLQEIKEQEYQAQVEEMRLMMNQLEEDLVSARRRSDLYESELRESRLAAEEF
HDIREQSRKLQEIKEQEYQAQVEEMRLMMNQLEEDLVSARRRSDLYESELRESRLAAEEF
HDIREQSRKLQEIKEQEYQAQVEEMRLMMNQLEEDLVSARRRSDLYESELRESRLAAEEF

KRKATECQHKLLKAKDQGKPEVGEYAKLEKINAEQQLKIQELQEKLEKAVKASTEATELL
KRKATECQHKLLKAKDQGKPEVGEYAKLEKINAEQQLKIQELQEKLEKAVKASTEATELL
KRKATECQHKLLKAKDQGKPEVGEYAKLEKINAEQQLKIQELQEKLEKAVKASTEATELL

QNIRQAKERAERELEKLQNREDSSEGIRKKLVEAEERRHSLENKVKRLETMERRENRLKD
QNIRQAKERAERELEKLQNREDSSEGIRKKLVEAEERRHSLENKVKRLETMERRENRLKD
QNIRQAKERAERELEKLQNREDSSEGIRKKLVEAEERRHSLENKVKRLETMERRENRLKD

DIQTKSQQIQQMADKILELEEKHREAQVSAQHLEVHLKQKEQHYYEKKIKVLDNQIKKDLA
DIQTKSQQIQQMADKILELEEKHREAQVSAQHLEVHLKQKEQHYYEKKIKVLDNQIKKDLA
DIQTKSQQIQQMADKILELEEKHREAQVSAQHLEVHLKQKEQHYYEKKIKVLDNQIKKDLA

DKETLENMMQRHEEEAHEKGKILSEQKAMINAMDSKIRSLEQRIVELSEANKLAANSSLF
DKETLENMMQRHEEEAHEKGKILSEQKAMINAMDSKIRSLEQRIVELSEANKLAANSSLF
DKETLENMMQRHEEEAHEKGKILSEQKAMINAMDSKIRSLEQRIVELSEANKLAANSSLF

TQRNMKAQEEMISELRQQKFYLETQAGKLEAQNRKLEEQLEKISHQDHSDKNRLLLELETR
TQRNMKAQEEMISELRQQKFYLETQAGKLEAQNRKLEEQLEKISHQDHSDKNRLLLELETR
TQRNMKAQEEMISELRQQKFYLETQAGKLEAQNRKLEEQLEKISHQDHSDKNRLLLELETR

LREVSLEHEEQKLELKRQLTELQLSLQERESQLTALQAARAALLESQLRQAKTELEETTAE
LREVSLEHEEQKLELKRQLTELQLSLQERESQLTALQAARAALLESQLRQAKTELEETTAE
LREVSLEHEEQKLELKRQLTELQLSLQERESQLTALQAARAALLESQLRQAKTELEETTAE

AAAAIQALTAHRDEIQRKFDALRNSCTVITDLEEQLNQLTEDNAELNNQNFYLSKQLDEA
AAAAIQALTAHRDEIQRKFDALRNSCTVITDLEEQLNQLTEDNAELNNQNFYLSKQLDEA
AAAAIQALTAHRDEIQRKFDALRNSCTVITDLEEQLNQLTEDNAELNNQNFYLSKQLDEA

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Fig. 22 (continued)

SGANDEIVQLRSEVDHLRREITEREMQLTSQKQTMEALKTTCTMLEEQVMDLEALNDELL
SGANDEIVQLRSEVDHLRREITEREMQLTSQKQTMEALKTTCTMLEEQVMDLEALNDELL
SGANDEIVQLRSEVDHLRREITEREMQLTSQKQTMEALKTTCTMLEEQVMDLEALNDELL

EKERQWEAWRSVLGDEKSQFECRVRELQRM LDTEKQSRARADQRITESRQVVELAVKEHK
EKERQWEAWRSVLGDEKSQFECRVRELQRM LDTEKQSRARADQRITESRQVVELAVKEHK
EKERQWEAWRSVLGDEKSQFECRVRELQRM LDTEKQSRARADQRITESRQVVELAVKEHK

AEILALQQALKEQKLKAESLSDKLNDEKKHAMLEMNARSLQQKLETERELKQRLLEEQA
AEILALQQALKEQKLKAESLSDKLNDEKKHAMLEMNARSLQQKLETERELKQRLLEEQA
AEILALQQALKEQKLKAESLSDKLNDEKKHAMLEMNARSLQQKLETERELKQRLLEEQA

KLQQQMDLQKNHIFRLTQGLQEALDRADLLKTERS DLEYQLENIQVLYSHEKVKMEGTIS
KLQQQMDLQKNHIFRLTQGLQEALDRADLLKTERS DLEYQLENIQVLYSHEKVKMEGTIS
KLQQQMDLQKNHIFRLTQGLQEALDRADLLKTERS DLEYQLENIQVLYSHEKVKMEGTIS

QQTKLIDFLQAKMDQPAKKKKVPLQYNELKLAL EKEKARCAELEEEALQKTRIELRSAREE
QQTKLIDFLQAKMDQPAKKKKVPLQYNELKLAL EKEKARCAELEEEALQKTRIELRSAREE
QQTKLIDFLQAKMDQPAKKKKVPLQYNELKLAL EKEKARCAELEEEALQKTRIELRSAREE

AAHRKATDHPHPSTPATARQQIAMS AIVRSPEHQPSAMSL LAPPSSRRKESSTPEEFSRR
AAHRKATDHPHPSTPATARQQIAMS AIVRSPEHQPSAMSL LAPPSSRRKESSTPEEFSRR
AAHRKATDHPHPSTPATARQQIAMS AIVRSPEHQPSAMSL LAPPSSRRKESSTPEEFSRR

LKERMHHNIPHRFNVGLNMRATKCAVCLDTVHFGRQASKCLECQVMCHPKCSTCLPATCG
LKERMHHNIPHRFNVGLNMRATKCAVCLDTVHFGRQASKCLECQVMCHPKCSTCLPATCG
LKERMHHNIPHRFNVGLNMRATKCAVCLDTVHFGRQASKCLECQVMCHPKCSTCLPATCG

LPAEYATHFTEAFCRDKMNSPGLQTKEPSSSLHLEGWMKVPRNNKRGQQGWDRKYIVLEG
LPAEYATHFTEAFCRDKMNSPGLQTKEPSSSLHLEGWMKVPRNNKRGQQGWDRKYIVLEG
LPAEYATHFTEAFCRDKMNSPGLQTKEPSSSLHLEGWMKVPRNNKRGQQGWDRKYIVLEG

SKVLIYDNEAREAGQRPVEEFELCLPDGDVSIHGAVGASELANTAKADVPIYILKMESH PH
SKVLIYDNEAREAGQRPVEEFELCLPDGDVSIHGAVGASELANTAKADVPIYILKMESH PH
SKVLIYDNEAREAGQRPVEEFELCLPDGDVSIHGAVGASELANTAKADVPIYILKMESH PH

TTCWPGR TLYLLAPSFPDKQRWVTALESV VAGGRVSREKAEADAKLLGNSLLKLEGDDRL
TTCWPGR TLYLLAPSFPDKQRWVTALESV VAGGRVSREKAEADAKLLGNSLLKLEGDDRL
TTCWPGR TLYLLAPSFPDKQRWVTALESV VAGGRVSREKAEADAKLLGNSLLKLEGDDRL

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Fig. 22 (continued)

DMNCTLPPFSDQVVLVGTEEGLYALNVLKNSLTHVPGIGAVFQIYI IKDLEKLLMIAGEER
DMNCTLPPFSDQVVLVGTEEGLYALNVLKNSLTHVPGIGAVFQIYI IKDLEKLLMIAGEER
DMNCTLPPFSDQVVLVGTEEGLYALNVLKNSLTHVPGIGAVFQIYI IKDLEKLLMIAGEER

ALCLVDVKKVKQSLAQSHLPAQPDISPNI FEAVKGCHLFGAGKIENGLCICAAMPSKVVI
ALCLVDVKKVKQSLAQSHLPAQPDISPNI FEAVKGCHLFGAGKIENGLCICAAMPSKVVI
ALCLVDVKKVKQSLAQSHLPAQPDISPNI FEAVKGCHLFGAGKIENGLCICAAMPSKVVI

LRYNENLSKYCIRKEIETSEPCSCIHFTNYSILIGTNKFYEIDMKQYTLEEF LDKNDHSL
LRYNENLSKYCIRKEIETSEPCSCIHFTNYSILIGTNKFYEIDMKQYTLEEF LDKNDHSL
LRYNENLSKYCIRKEIETSEPCSCIHFTNYSILIGTNKFYEIDMKQYTLEEF LDKNDHSL

APAVFAASSNSFPVSIVQVNSAGQREEYLLCFHEFGVFVDSYGRRSRTDDLKWSRLPLAF
APAVFAASSNSFPVSIVQVNSAGQREEYLLCFHEFGVFVDSYGRRSRTDDLKWSRLPLAF
APAVFAASSNSFPVSIVQVNSAGQREEYLLCFHEFGVFVDSYGRRSRTDDLKWSRLPLAF

AYREPYL FVTHFNSLEVIEIQARSSAGTPARAYLDIPNPRYLGP AISSGAIY LASSYQDK
AYREPYL FVTHFNSLEVIEIQARSSAGTPARAYLDIPNPRYLGP AISSGAIY LASSYQDK
AYREPYL FVTHFNSLEVIEIQARSSAGTPARAYLDIPNPRYLGP AISSGAIY LASSYQDK

LRVICCKGNLVKESGTEHHRGPSTSRSSPNKRGPP TYNEHITKRVASSAPPEG PSHPRE
LRVICCKGNLVKESGTEHHRGPSTSRSSPNKRGPP TYNEHITKRVASSAPPEG PSHPRE
LRVICCKGNLVKESGTEHHRGPSTSRSSPNKRGPP TYNEHITKRVASSAPPEG PSHPRE

PSTPHRYREGRT ELRRDKSPGRPLEREKSPGRMLSTRRERSPGRLFEDSSRGRLPAGAVR
PSTPHRYREGRT ELRRDKSPGRPLEREKSPGRMLSTRRERSPGRLFEDSSRGRLPAGAVR
PSTPHRYREGRT ELRRDKSPGRPLEREKSPGRMLSTRRERSPGRLFEDSSRGRLPAGAVR

TPLSQVNKVWDQS 2052

TPLSQVNKV . . S

TPLSQVNKVRQHS 6159

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Fig. 23

TBLASTN - alignment of 543_Protein against BAYER_LIB_DNA|wu_373006001280181
Bayer Corp Pharma Proprietary OP Library: Fat Rat Hypothalamus Linda Wu Fr
Oct 15 15:45:51 EDT 1999

This hit is scoring at : 2e-37 (expectation value)
Alignment length (overlap) : 77
Identities : 100 %
Scoring matrix : BLOSUM62 (used to infer consensus pattern)
Hit reading frame : -3
Database searched : bayerall_1_;

Q: 964 IQALTAHRDEIQRKFDALRNSCTVITDLEEQLNQLTEDNAELNNQNFYLSKQLDEASGAN
IQALTAHRDEIQRKFDALRNSCTVITDLEEQLNQLTEDNAELNNQNFYLSKQLDEASGAN
H: 231 IQALTAHRDEIQRKFDALRNSCTVITDLEEQLNQLTEDNAELNNQNFYLSKQLDEASGAN

DEIVQLRSEVDHLRREI 1040
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Fig. 24

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CAGCAGATGTCTCCTCTTTCCCGAGAAGGGATATTAGATGCCCTCTTTGTTCTCTTTGAA
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Fig. 24 (continued)

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Fig. 24 (continued)

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<151> 2002-04-25

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625 630 635 640

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Leu Gln Glu Lys Leu Glu Lys Ala Val Lys Ala Ser Thr Glu Ala Thr
645 650 655

Glu Leu Leu Gln Asn Ile Arg Gln Ala Lys Glu Arg Ala Glu Arg Glu
660 665 670

Leu Glu Lys Leu Gln Asn Arg Glu Asp Ser Ser Glu Gly Ile Arg Lys
675 680 685

Lys Leu Val Glu Ala Glu Glu Arg Arg His Ser Leu Glu Asn Lys Val
690 695 700

Lys Arg Leu Glu Thr Met Glu Arg Arg Glu Asn Arg Leu Lys Asp Asp
705 710 715 720

Ile Gln Thr Lys Ser Gln Gln Ile Gln Gln Met Ala Asp Lys Ile Leu
725 730 735

Glu Leu Glu Glu Lys His Arg Glu Ala Gln Val Ser Ala Gln His Leu
740 745 750

Glu Val His Leu Lys Gln Lys Glu Gln His Tyr Glu Glu Lys Ile Lys
755 760 765

Val Leu Asp Asn Gln Ile Lys Lys Asp Leu Ala Asp Lys Glu Thr Leu
770 775 780

Glu Asn Met Met Gln Arg His Glu Glu Glu Ala His Glu Lys Gly Lys
785 790 795 800

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Ile Leu Ser Glu Gln Lys Ala Met Ile Asn Ala Met Asp Ser Lys Ile
805 810 815

Arg Ser Leu Glu Gln Arg Ile Val Glu Leu Ser Glu Ala Asn Lys Leu
820 825 830

Ala Ala Asn Ser Ser Leu Phe Thr Gln Arg Asn Met Lys Ala Gln Glu
835 840 845

Glu Met Ile Ser Glu Leu Arg Gln Gln Lys Phe Tyr Leu Glu Thr Gln
850 855 860

Ala Gly Lys Leu Glu Ala Gln Asn Arg Lys Leu Glu Glu Gln Leu Glu
865 870 875 880

Lys Ile Ser His Gln Asp His Ser Asp Lys Asn Arg Leu Leu Glu Leu
885 890 895

Glu Thr Arg Leu Arg Glu Val Ser Leu Glu His Glu Glu Gln Lys Leu
900 905 910

Glu Leu Lys Arg Gln Leu Thr Glu Leu Gln Leu Ser Leu Gln Glu Arg
915 920 925

Glu Ser Gln Leu Thr Ala Leu Gln Ala Ala Arg Ala Ala Leu Glu Ser
930 935 940

Gln Leu Arg Gln Ala Lys Thr Glu Leu Glu Glu Thr Thr Ala Glu Ala
945 950 955 960

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Glu Glu Glu Ile Gln Ala Leu Thr Ala His Arg Asp Glu Ile Gln Arg
965 970 975

Lys Phe Asp Ala Leu Arg Asn Ser Cys Thr Val Ile Thr Asp Leu Glu
980 985 990

Glu Gln Leu Asn Gln Leu Thr Glu Asp Asn Ala Glu Leu Asn Asn Gln
995 1000 1005

Asn Phe Tyr Leu Ser Lys Gln Leu Asp Glu Ala Ser Gly Ala Asn
1010 1015 1020

Asp Glu Ile Val Gln Leu Arg Ser Glu Val Asp His Leu Arg Arg
1025 1030 1035

Glu Ile Thr Glu Arg Glu Met Gln Leu Thr Ser Gln Lys Gln Thr
1040 1045 1050

Met Glu Ala Leu Lys Thr Thr Cys Thr Met Leu Glu Glu Gln Val
1055 1060 1065

Met Asp Leu Glu Ala Leu Asn Asp Glu Leu Leu Glu Lys Glu Arg
1070 1075 1080

Gln Trp Glu Ala Trp Arg Ser Val Leu Gly Asp Glu Lys Ser Gln
1085 1090 1095

Phe Glu Cys Arg Val Arg Glu Leu Gln Arg Met Leu Asp Thr Glu
1100 1105 1110

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Lys	Gln	Ser	Arg	Ala	Arg	Ala	Asp	Gln	Arg	Ile	Thr	Glu	Ser	Arg
1115						1120					1125			

Gln	Val	Val	Glu	Leu	Ala	Val	Lys	Glu	His	Lys	Ala	Glu	Ile	Leu
1130						1135					1140			

Ala	Leu	Gln	Gln	Ala	Leu	Lys	Glu	Gln	Lys	Leu	Lys	Ala	Glu	Ser
1145						1150					1155			

Leu	Ser	Asp	Lys	Leu	Asn	Asp	Leu	Glu	Lys	Lys	His	Ala	Met	Leu
1160						1165					1170			

Glu	Met	Asn	Ala	Arg	Ser	Leu	Gln	Gln	Lys	Leu	Glu	Thr	Glu	Arg
1175						1180					1185			

Glu	Leu	Lys	Gln	Arg	Leu	Leu	Glu	Glu	Gln	Ala	Lys	Leu	Gln	Gln
1190						1195					1200			

Gln	Met	Asp	Leu	Gln	Lys	Asn	His	Ile	Phe	Arg	Leu	Thr	Gln	Gly
1205						1210					1215			

Leu	Gln	Glu	Ala	Leu	Asp	Arg	Ala	Asp	Leu	Leu	Lys	Thr	Glu	Arg
1220						1225					1230			

Ser	Asp	Leu	Glu	Tyr	Gln	Leu	Glu	Asn	Ile	Gln	Val	Leu	Tyr	Ser
1235						1240					1245			

His	Glu	Lys	Val	Lys	Met	Glu	Gly	Thr	Ile	Ser	Gln	Gln	Thr	Lys
1250						1255					1260			

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Leu Ile Asp Phe Leu Gln Ala Lys Met Asp Gln Pro Ala Lys Lys
1265 1270 1275

Lys Lys Val Pro Leu Gln Tyr Asn Glu Leu Lys Leu Ala Leu Glu
1280 1285 1290

Lys Glu Lys Ala Arg Cys Ala Glu Leu Glu Glu Ala Leu Gln Lys
1295 1300 1305

Thr Arg Ile Glu Leu Arg Ser Ala Arg Glu Glu Ala Ala His Arg
1310 1315 1320

Lys Ala Thr Asp His Pro His Pro Ser Thr Pro Ala Thr Ala Arg
1325 1330 1335

Gln Gln Ile Ala Met Ser Ala Ile Val Arg Ser Pro Glu His Gln
1340 1345 1350

Pro Ser Ala Met Ser Leu Leu Ala Pro Pro Ser Ser Arg Arg Lys
1355 1360 1365

Glu Ser Ser Thr Pro Glu Glu Phe Ser Arg Arg Leu Lys Glu Arg
1370 1375 1380

Met His His Asn Ile Pro His Arg Phe Asn Val Gly Leu Asn Met
1385 1390 1395

Arg Ala Thr Lys Cys Ala Val Cys Leu Asp Thr Val His Phe Gly
1400 1405 1410

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Arg	Gln	Ala	Ser	Lys	Cys	Leu	Glu	Cys	Gln	Val	Met	Cys	His	Pro
1415						1420					1425			

Lys	Cys	Ser	Thr	Cys	Leu	Pro	Ala	Thr	Cys	Gly	Leu	Pro	Ala	Glu
1430						1435					1440			

Tyr	Ala	Thr	His	Phe	Thr	Glu	Ala	Phe	Cys	Arg	Asp	Lys	Met	Asn
1445						1450					1455			

Ser	Pro	Gly	Leu	Gln	Thr	Lys	Glu	Pro	Ser	Ser	Ser	Leu	His	Leu
1460						1465					1470			

Glu	Gly	Trp	Met	Lys	Val	Pro	Arg	Asn	Asn	Lys	Arg	Gly	Gln	Gln
1475						1480					1485			

Gly	Trp	Asp	Arg	Lys	Tyr	Ile	Val	Leu	Glu	Gly	Ser	Lys	Val	Leu
1490						1495					1500			

Ile	Tyr	Asp	Asn	Glu	Ala	Arg	Glu	Ala	Gly	Gln	Arg	Pro	Val	Glu
1505						1510					1515			

Glu	Phe	Glu	Leu	Cys	Leu	Pro	Asp	Gly	Asp	Val	Ser	Ile	His	Gly
1520						1525					1530			

Ala	Val	Gly	Ala	Ser	Glu	Leu	Ala	Asn	Thr	Ala	Lys	Ala	Asp	Val
1535						1540					1545			

Pro	Tyr	Ile	Leu	Lys	Met	Glu	Ser	His	Pro	His	Thr	Thr	Cys	Trp
1550						1555					1560			

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Pro Gly Arg Thr Leu Tyr Leu Leu Ala Pro Ser Phe Pro Asp Lys
1565 1570 1575

Gln Arg Trp Val Thr Ala Leu Glu Ser Val Val Ala Gly Gly Arg
1580 1585 1590

Val Ser Arg Glu Lys Ala Glu Ala Asp Ala Lys Leu Leu Gly Asn
1595 1600 1605

Ser Leu Leu Lys Leu Glu Gly Asp Asp Arg Leu Asp Met Asn Cys
1610 1615 1620

Thr Leu Pro Phe Ser Asp Gln Val Val Leu Val Gly Thr Glu Glu
1625 1630 1635

Gly Leu Tyr Ala Leu Asn Val Leu Lys Asn Ser Leu Thr His Val
1640 1645 1650

Pro Gly Ile Gly Ala Val Phe Gln Ile Tyr Ile Ile Lys Asp Leu
1655 1660 1665

Glu Lys Leu Leu Met Ile Ala Gly Glu Glu Arg Ala Leu Cys Leu
1670 1675 1680

Val Asp Val Lys Lys Val Lys Gln Ser Leu Ala Gln Ser His Leu
1685 1690 1695

Pro Ala Gln Pro Asp Ile Ser Pro Asn Ile Phe Glu Ala Val Lys
1700 1705 1710

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Gly Cys	His Leu Phe Gly Ala	Gly Lys Ile Glu Asn	Gly Leu Cys
1715	1720	1725	

Ile Cys	Ala Ala Met Pro Ser	Lys Val Val Ile Leu	Arg Tyr Asn
1730	1735	1740	

Glu Asn	Leu Ser Lys Tyr Cys	Ile Arg Lys Glu Ile	Glu Thr Ser
1745	1750	1755	

Glu Pro	Cys Ser Cys Ile His	Phe Thr Asn Tyr Ser	Ile Leu Ile
1760	1765	1770	

Gly Thr	Asn Lys Phe Tyr Glu	Ile Asp Met Lys Gln	Tyr Thr Leu
1775	1780	1785	

Glu Glu	Phe Leu Asp Lys Asn	Asp His Ser Leu Ala	Pro Ala Val
1790	1795	1800	

Phe Ala	Ala Ser Ser Asn Ser	Phe Pro Val Ser Ile	Val Gln Val
1805	1810	1815	

Asn Ser	Ala Gly Gln Arg Glu	Glu Tyr Leu Leu Cys	Phe His Glu
1820	1825	1830	

Phe Gly	Val Phe Val Asp Ser	Tyr Gly Arg Arg Ser	Arg Thr Asp
1835	1840	1845	

Asp Leu	Lys Trp Ser Arg Leu	Pro Leu Ala Phe Ala	Tyr Arg Glu
1850	1855	1860	

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Pro	Tyr	Leu	Phe	Val	Thr	His	Phe	Asn	Ser	Leu	Glu	Val	Ile	Glu
1865						1870					1875			

Ile	Gln	Ala	Arg	Ser	Ser	Ala	Gly	Thr	Pro	Ala	Arg	Ala	Tyr	Leu
1880						1885					1890			

Asp	Ile	Pro	Asn	Pro	Arg	Tyr	Leu	Gly	Pro	Ala	Ile	Ser	Ser	Gly
1895						1900					1905			

Ala	Ile	Tyr	Leu	Ala	Ser	Ser	Tyr	Gln	Asp	Lys	Leu	Arg	Val	Ile
1910						1915					1920			

Cys	Cys	Lys	Gly	Asn	Leu	Val	Lys	Glu	Ser	Gly	Thr	Glu	His	His
1925						1930					1935			

Arg	Gly	Pro	Ser	Thr	Ser	Arg	Ser	Ser	Pro	Asn	Lys	Arg	Gly	Pro
1940						1945					1950			

Pro	Thr	Tyr	Asn	Glu	His	Ile	Thr	Lys	Arg	Val	Ala	Ser	Ser	Pro
1955						1960					1965			

Ala	Pro	Pro	Glu	Gly	Pro	Ser	His	Pro	Arg	Glu	Pro	Ser	Thr	Pro
1970						1975					1980			

His	Arg	Tyr	Arg	Glu	Gly	Arg	Thr	Glu	Leu	Arg	Arg	Asp	Lys	Ser
1985						1990					1995			

Pro	Gly	Arg	Pro	Leu	Glu	Arg	Glu	Lys	Ser	Pro	Gly	Arg	Met	Leu
2000						2005					2010			

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Ser Thr Arg Arg Glu Arg Ser Pro Gly Arg Leu Phe Glu Asp Ser
2015 2020 2025

Ser Arg Gly Arg Leu Pro Ala Gly Ala Val Arg Thr Pro Leu Ser
2030 2035 2040

Gln Val Asn Lys Val Trp Asp Gln Ser Ser Val
2045 2050

<210> 3
<211> 2055
<212> PRT
<213> Homo sapiens

<400> 3

Met Leu Lys Phe Lys Tyr Gly Val Arg Asn Pro Pro Glu Ala Ser Ala
1 5 10 15

Ser Glu Pro Ile Ala Ser Arg Ala Ser Arg Leu Asn Leu Phe Phe Gln
20 25 30

Gly Lys Pro Pro Leu Met Thr Gln Gln Gln Met Ser Ala Leu Ser Arg
35 40 45

Glu Gly Met Leu Asp Ala Leu Phe Ala Leu Phe Glu Glu Cys Ser Gln
50 55 60

Pro Ala Leu Met Lys Met Lys His Val Ser Ser Phe Val Gln Lys Tyr
65 70 75 80

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Ser Asp Thr Ile Ala Glu Leu Arg Glu Leu Gln Pro Ser Ala Arg Asp
85 90 95

Phe Glu Val Arg Ser Leu Val Gly Cys Gly His Phe Ala Glu Val Gln
100 105 110

Val Val Arg Glu Lys Ala Thr Gly Asp Val Tyr Ala Met Lys Ile Met
115 120 125

Lys Lys Lys Ala Leu Leu Ala Gln Glu Gln Val Ser Phe Phe Glu Glu
130 135 140

Glu Arg Asn Ile Leu Ser Arg Ser Thr Ser Pro Trp Ile Pro Gln Leu
145 150 155 160

Gln Tyr Ala Phe Gln Asp Lys Asn Asn Leu Tyr Leu Val Met Glu Tyr
165 170 175

Gln Pro Gly Gly Asp Phe Leu Ser Leu Leu Asn Arg Tyr Glu Asp Gln
180 185 190

Leu Asp Glu Ser Met Ile Gln Phe Tyr Leu Ala Glu Leu Ile Leu Ala
195 200 205

Val His Ser Val His Gln Met Gly Tyr Val His Arg Asp Ile Lys Pro
210 215 220

Glu Asn Ile Leu Ile Asp Arg Thr Gly Glu Ile Lys Leu Val Asp Phe
225 230 235 240

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Gly Ser Ala Ala Lys Met Asn Ser Asn Lys Val Asp Ala Lys Leu Pro
245 250 255

Ile Gly Thr Pro Asp Tyr Met Ala Pro Glu Val Leu Thr Val Met Asn
260 265 270

Glu Asp Arg Arg Gly Thr Tyr Gly Leu Asp Cys Asp Trp Trp Ser Val
275 280 285

Gly Val Val Ala Tyr Glu Met Val Tyr Gly Lys Thr Pro Phe Thr Glu
290 295 300

Gly Thr Ser Ala Arg Thr Phe Asn Asn Ile Met Asn Phe Gln Arg Phe
305 310 315 320

Leu Lys Phe Pro Asp Asp Pro Lys Val Ser Ser Glu Leu Leu Asp Leu
325 330 335

Leu Gln Ser Leu Leu Cys Val Gln Lys Glu Arg Leu Lys Phe Glu Gly
340 345 350

Leu Cys Cys His Pro Phe Phe Ala Arg Thr Asp Trp Asn Asn Ile Arg
355 360 365

Asn Ser Pro Pro Pro Phe Val Pro Thr Leu Lys Ser Asp Asp Asp Thr
370 375 380

Ser Asn Phe Asp Glu Pro Glu Lys Asn Ser Trp Ala Phe Ile Leu Cys
385 390 395 400

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Val Pro Ala Glu Pro Leu Ala Phe Ser Gly Glu Glu Leu Pro Phe Val
405 410 415

Gly Phe Ser Tyr Ser Lys Ala Leu Gly Tyr Leu Gly Arg Ser Glu Ser
420 425 430

Val Val Ser Ser Leu Asp Ser Pro Ala Lys Val Ser Ser Met Glu Lys
435 440 445

Lys Leu Leu Ile Lys Ser Lys Glu Leu Gln Asp Ser Gln Asp Lys Cys
450 455 460

His Lys Met Glu Gln Glu Met Thr Arg Leu His Arg Arg Val Ser Glu
465 470 475 480

Val Glu Ala Val Leu Ser Gln Lys Glu Val Glu Leu Lys Ala Ser Glu
485 490 495

Thr Gln Arg Ser Leu Leu Glu Gln Asp Leu Ala Thr Tyr Ile Thr Glu
500 505 510

Cys Ser Ser Leu Lys Arg Ser Leu Glu Gln Ala Arg Met Glu Val Ser
515 520 525

Gln Glu Asp Asp Lys Ala Leu Gln Leu Leu His Asp Ile Arg Glu Gln
530 535 540

Ser Arg Lys Leu Gln Glu Ile Lys Glu Gln Glu Tyr Gln Ala Gln Val
545 550 555 560

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Glu Glu Met Arg Leu Met Met Asn Gln Leu Glu Glu Asp Leu Val Ser
565 570 575

Ala Arg Arg Arg Ser Asp Leu Tyr Glu Ser Glu Leu Arg Glu Ser Arg
580 585 590

Leu Ala Ala Glu Glu Phe Lys Arg Lys Ala Asn Glu Cys Gln His Lys
595 600 605

Leu Met Lys Ala Lys Asp Gln Gly Lys Pro Glu Val Gly Glu Tyr Ser
610 615 620

Lys Leu Glu Lys Ile Asn Ala Glu Gln Gln Leu Lys Ile Gln Glu Leu
625 630 635 640

Gln Glu Lys Leu Glu Lys Ala Val Lys Ala Ser Thr Glu Ala Thr Glu
645 650 655

Leu Leu Gln Asn Ile Arg Gln Ala Lys Glu Arg Ala Glu Arg Glu Leu
660 665 670

Glu Lys Leu His Asn Arg Glu Asp Ser Ser Glu Gly Ile Lys Lys Lys
675 680 685

Leu Val Glu Ala Glu Glu Arg Arg His Ser Leu Glu Asn Lys Val Lys
690 695 700

Arg Leu Glu Thr Met Glu Arg Arg Glu Asn Arg Leu Lys Asp Asp Ile
705 710 715 720

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Gln Thr Lys Ser Glu Gln Ile Gln Gln Met Ala Asp Lys Ile Leu Glu
725 730 735

Leu Glu Glu Lys His Arg Glu Ala Gln Val Ser Ala Gln His Leu Glu
740 745 750

Val His Leu Lys Gln Lys Glu Gln His Tyr Glu Glu Lys Ile Lys Val
755 760 765

Leu Asp Asn Gln Ile Lys Lys Asp Leu Ala Asp Lys Glu Ser Leu Glu
770 775 780

Asn Met Met Gln Arg His Glu Glu Glu Ala His Glu Lys Gly Lys Ile
785 790 795 800

Leu Ser Glu Gln Lys Ala Met Ile Asn Ala Met Asp Ser Lys Ile Arg
805 810 815

Ser Leu Glu Gln Arg Ile Val Glu Leu Ser Glu Ala Asn Lys Leu Ala
820 825 830

Ala Asn Ser Ser Leu Phe Thr Gln Arg Asn Met Lys Ala Gln Glu Glu
835 840 845

Met Ile Ser Glu Leu Arg Gln Gln Lys Phe Tyr Leu Glu Thr Gln Ala
850 855 860

Gly Lys Leu Glu Ala Gln Asn Arg Lys Leu Glu Glu Gln Leu Glu Lys
865 870 875 880

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Ile Ser His Gln Asp His Ser Asp Lys Ser Arg Leu Leu Glu Leu Glu
885 890 895

Thr Arg Leu Arg Glu Val Ser Leu Glu His Glu Glu Gln Lys Leu Glu
900 905 910

Leu Lys Arg Gln Leu Thr Glu Leu Gln Leu Ser Leu Gln Glu Arg Glu
915 920 925

Ser Gln Leu Thr Ala Leu Gln Ala Ala Arg Ala Ala Leu Glu Ser Gln
930 935 940

Leu Arg Gln Ala Lys Thr Glu Leu Glu Glu Thr Thr Ala Glu Ala Glu
945 950 955 960

Glu Glu Ile Gln Ala Leu Thr Ala His Arg Asp Glu Ile Gln Arg Lys
965 970 975

Phe Asp Ala Leu Arg Asn Ser Cys Thr Val Ile Thr Asp Leu Glu Glu
980 985 990

Gln Leu Asn Gln Leu Thr Glu Asp Asn Ala Glu Leu Asn Asn Gln Asn
995 1000 1005

Phe Tyr Leu Ser Lys Gln Leu Asp Glu Ala Ser Gly Ala Asn Asp
1010 1015 1020

Glu Ile Val Gln Leu Arg Ser Glu Val Asp His Leu Arg Arg Glu
1025 1030 1035

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Ile Thr	Glu Arg	Glu Met	Gln	Leu Thr	Ser	Gln Lys	Gln Thr Met
1040			1045			1050	

Glu Ala	Leu Lys	Thr Thr	Cys	Thr Met	Leu Glu	Glu	Gln Val Leu
1055			1060			1065	

Asp Leu	Glu Ala	Leu Asn	Asp	Glu Leu	Leu Glu	Lys	Glu Arg Gln
1070			1075			1080	

Trp Glu	Ala Trp	Arg Ser	Val	Leu Gly	Asp Glu	Lys	Ser Gln Phe
1085			1090			1095	

Glu Cys	Arg Val	Arg Glu	Leu	Gln Arg	Met Leu	Asp	Thr Glu Lys
1100			1105			1110	

Gln Ser	Arg Ala	Arg Ala	Asp	Gln Arg	Ile Thr	Glu	Ser Arg Gln
1115			1120			1125	

Val Val	Glu Leu	Ala Val	Lys	Glu His	Lys Ala	Glu	Ile Leu Ala
1130			1135			1140	

Leu Gln	Gln Ala	Leu Lys	Glu	Gln Lys	Leu Lys	Ala	Glu Ser Leu
1145			1150			1155	

Ser Asp	Lys Leu	Asn Asp	Leu	Glu Lys	Lys His	Ala	Met Leu Glu
1160			1165			1170	

Met Asn	Ala Arg	Ser Leu	Gln	Gln Lys	Leu Glu	Thr	Glu Arg Glu
1175			1180			1185	

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Leu Lys Gln Arg Leu Leu Glu Glu Gln Ala Lys Leu Gln Gln Gln
1190 1195 1200

Met Asp Leu Gln Lys Asn His Ile Phe Arg Leu Thr Gln Gly Leu
1205 1210 1215

Gln Glu Ala Leu Asp Arg Ala Asp Leu Leu Lys Thr Glu Arg Ser
1220 1225 1230

Asp Leu Glu Tyr Gln Leu Glu Asn Ile Gln Val Leu Tyr Ser His
1235 1240 1245

Glu Lys Val Lys Met Glu Gly Thr Ile Ser Gln Gln Thr Lys Leu
1250 1255 1260

Ile Asp Phe Leu Gln Ala Lys Met Asp Gln Pro Ala Lys Lys Lys
1265 1270 1275

Lys Val Pro Leu Gln Tyr Asn Glu Leu Lys Leu Ala Leu Glu Lys
1280 1285 1290

Glu Lys Ala Arg Cys Ala Glu Leu Glu Glu Ala Leu Gln Lys Thr
1295 1300 1305

Arg Ile Glu Leu Arg Ser Ala Arg Glu Glu Ala Ala His Arg Lys
1310 1315 1320

Ala Thr Asp His Pro His Pro Ser Thr Pro Ala Thr Ala Arg Gln
1325 1330 1335

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Gln Ile Ala Met Ser Ala Ile Val Arg Ser Pro Glu His Gln Pro
1340 1345 1350

Ser Ala Met Ser Leu Leu Ala Pro Pro Ser Ser Arg Arg Lys Glu
1355 1360 1365

Ser Ser Thr Pro Glu Glu Phe Ser Arg Arg Leu Lys Glu Arg Met
1370 1375 1380

His His Asn Ile Pro His Arg Phe Asn Val Gly Leu Asn Met Arg
1385 1390 1395

Ala Thr Lys Cys Ala Val Cys Leu Asp Thr Val His Phe Gly Arg
1400 1405 1410

Gln Ala Ser Lys Cys Leu Glu Cys Gln Val Met Cys His Pro Lys
1415 1420 1425

Cys Ser Thr Cys Leu Pro Ala Thr Cys Gly Leu Pro Ala Glu Tyr
1430 1435 1440

Ala Thr His Phe Thr Glu Ala Phe Cys Arg Asp Lys Met Asn Ser
1445 1450 1455

Pro Gly Leu Gln Ser Lys Glu Pro Gly Ser Ser Leu His Leu Glu
1460 1465 1470

Gly Trp Met Lys Val Pro Arg Asn Asn Lys Arg Gly Gln Gln Gly
1475 1480 1485

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Trp	Asp	Arg	Lys	Tyr	Ile	Val	Leu	Glu	Gly	Ser	Lys	Val	Leu	Ile
1490						1495					1500			

Tyr	Asp	Asn	Glu	Ala	Arg	Glu	Ala	Gly	Gln	Arg	Pro	Val	Glu	Glu
1505						1510					1515			

Phe	Glu	Leu	Cys	Leu	Pro	Asp	Gly	Asp	Val	Ser	Ile	His	Gly	Ala
1520						1525					1530			

Val	Gly	Ala	Ser	Glu	Leu	Ala	Asn	Thr	Ala	Lys	Ala	Asp	Val	Pro
1535						1540					1545			

Tyr	Ile	Leu	Lys	Met	Glu	Ser	His	Pro	His	Thr	Thr	Cys	Trp	Pro
1550						1555					1560			

Gly	Arg	Thr	Leu	Tyr	Leu	Leu	Ala	Pro	Ser	Phe	Pro	Asp	Lys	Gln
1565						1570					1575			

Arg	Trp	Val	Thr	Ala	Leu	Glu	Ser	Val	Val	Ala	Gly	Gly	Arg	Val
1580						1585					1590			

Ser	Arg	Glu	Lys	Ala	Glu	Ala	Asp	Ala	Lys	Leu	Leu	Gly	Asn	Ser
1595						1600					1605			

Leu	Leu	Lys	Leu	Glu	Gly	Asp	Asp	Arg	Leu	Asp	Met	Asn	Cys	Thr
1610						1615					1620			

Leu	Pro	Phe	Ser	Asp	Gln	Val	Val	Leu	Val	Gly	Thr	Glu	Glu	Gly
1625						1630					1635			

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Leu	Tyr	Ala	Leu	Asn	Val	Leu	Lys	Asn	Ser	Leu	Thr	His	Ile	Pro
1640						1645					1650			

Gly	Ile	Gly	Ala	Val	Phe	Gln	Ile	Tyr	Ile	Ile	Lys	Asp	Leu	Glu
1655						1660					1665			

Lys	Leu	Leu	Met	Ile	Ala	Gly	Glu	Glu	Arg	Ala	Leu	Cys	Leu	Val
1670						1675					1680			

Asp	Val	Lys	Lys	Val	Lys	Gln	Ser	Leu	Ala	Gln	Ser	His	Leu	Pro
1685						1690					1695			

Ala	Gln	Pro	Asp	Val	Ser	Pro	Asn	Ile	Phe	Glu	Ala	Val	Lys	Gly
1700						1705					1710			

Cys	His	Leu	Phe	Ala	Ala	Gly	Lys	Ile	Glu	Asn	Ser	Leu	Cys	Ile
1715						1720					1725			

Cys	Ala	Ala	Met	Pro	Ser	Lys	Val	Val	Ile	Leu	Arg	Tyr	Asn	Asp
1730						1735					1740			

Asn	Leu	Ser	Lys	Tyr	Cys	Ile	Arg	Lys	Glu	Ile	Glu	Thr	Ser	Glu
1745						1750					1755			

Pro	Cys	Ser	Cys	Ile	His	Phe	Thr	Asn	Tyr	Ser	Ile	Leu	Ile	Gly
1760						1765					1770			

Thr	Asn	Lys	Phe	Tyr	Glu	Ile	Asp	Met	Lys	Gln	Tyr	Thr	Leu	Asp
1775						1780					1785			

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Glu	Phe	Leu	Asp	Lys	Asn	Asp	His	Ser	Leu	Ala	Pro	Ala	Val	Phe
1790						1795					1800			

Ala	Ser	Ser	Ser	Asn	Ser	Phe	Pro	Val	Ser	Ile	Val	Gln	Ala	Asn
1805						1810					1815			

Ser	Ala	Gly	Gln	Arg	Glu	Glu	Tyr	Leu	Leu	Cys	Phe	His	Glu	Phe
1820						1825					1830			

Gly	Val	Phe	Val	Asp	Ser	Tyr	Gly	Arg	Arg	Ser	Arg	Thr	Asp	Asp
1835						1840					1845			

Leu	Lys	Trp	Ser	Arg	Leu	Pro	Leu	Ala	Phe	Ala	Tyr	Arg	Glu	Pro
1850						1855					1860			

Tyr	Leu	Phe	Val	Thr	His	Phe	Asn	Ser	Leu	Glu	Val	Ile	Glu	Ile
1865						1870					1875			

Gln	Ala	Arg	Ser	Ser	Leu	Gly	Ser	Pro	Ala	Arg	Ala	Tyr	Leu	Glu
1880						1885					1890			

Ile	Pro	Asn	Pro	Arg	Tyr	Leu	Gly	Pro	Ala	Ile	Ser	Ser	Gly	Ala
1895						1900					1905			

Ile	Tyr	Leu	Ala	Ser	Ser	Tyr	Gln	Asp	Lys	Leu	Arg	Val	Ile	Cys
1910						1915					1920			

Cys	Lys	Gly	Asn	Leu	Val	Lys	Glu	Ser	Gly	Thr	Glu	Gln	His	Arg
1925						1930					1935			

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Val	Pro	Ser	Thr	Ser	Arg	Ser	Ser	Pro	Asn	Lys	Arg	Gly	Pro	Pro
1940						1945					1950			

Thr	Tyr	Asn	Glu	His	Ile	Thr	Lys	Arg	Val	Ala	Ser	Ser	Pro	Ala
1955						1960					1965			

Pro	Pro	Glu	Gly	Pro	Ser	His	Pro	Arg	Glu	Pro	Ser	Thr	Pro	His
1970						1975					1980			

Arg	Tyr	Arg	Asp	Arg	Glu	Gly	Arg	Thr	Glu	Leu	Arg	Arg	Asp	Lys
1985						1990					1995			

Ser	Pro	Gly	Arg	Pro	Leu	Glu	Arg	Glu	Lys	Ser	Pro	Gly	Arg	Met
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2015						2020					2025			

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Arg Ser Leu Glu Gln Arg Ile Val Glu Leu Ser Glu Ala Asn Lys Leu
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Ala Ala Asn Ser Ser Leu Phe Thr Gln Arg Asn Met Lys Ala Gln Glu
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- 42 -

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Gln Leu Arg Gln Ala Lys Thr Glu Leu Glu Glu Thr Thr Ala Glu Ala
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Glu Glu Glu Ile Gln Ala Leu Thr Ala His Arg Asp Glu Ile Gln Arg
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Lys Phe Asp Ala Leu Arg Asn Ser Cys Thr Val Ile Thr Asp Leu Glu
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Glu Gln Leu Asn Gln Leu Thr Glu Asp Asn Ala Glu Leu Asn Asn Gln
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Glu Ile Val Gln Leu Arg Ser Glu Val Asp His Leu Arg Arg Glu Ile
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- 43 -

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Arg Ser Val Leu Gly Asp Glu Lys Ser Gln Phe Glu Cys Arg Val Arg
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Glu Leu Gln Arg Met Leu Asp Thr Glu Lys Gln Ser Arg Ala Arg Ala
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Asp Gln Arg Ile Thr Glu Ser Arg Gln Val Val Glu Leu Ala Val Lys
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370 375 380

Lys Leu Lys Ala Glu Ser Leu Ser Asp Lys Leu Asn Asp Leu Glu Lys
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Lys His Ala Met Leu Glu Met Asn Ala Arg Ser Leu Gln Gln Lys Leu
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- 44 -

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Ile Asp Phe Leu Gln Ala Lys Met Asp Gln Pro Ala Lys Lys Lys Lys
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Val Pro Leu Gln Tyr Asn Glu Leu Lys Leu Ala Leu Glu Lys Glu Lys
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Pro Ala Glu Tyr Ala Thr His Phe Thr Glu Ala Phe Cys Arg Asp Lys
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785 790 795 800

Tyr Leu Leu Ala Pro Ser Phe Pro Asp Lys Gln Arg Trp Val Thr Ala
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Ala Asp Ala Lys Leu Leu Gly Asn Ser Leu Leu Lys Leu Glu Gly Asp
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- 47 -

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- 48 -

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INTERNATIONAL SEARCH REPORT

International Application No
PCT/EP 02/07156

A. CLASSIFICATION OF SUBJECT MATTER

IPC 7 C07K14/435 C12N15/52 C12N5/10 C12N9/00 C12Q1/68
G01N33/53 G01N33/573 A61P9/10

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7 C07K C12N C12Q G01N A61P

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

EPO-Internal, BIOSIS, SEQUENCE SEARCH, PAJ, WPI Data

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 01 38503 A (PLOWMAN GREGORY D ;CLARY DOUGLAS (US); SUGEN INC (US); WHYTE DAVID) 31 May 2001 (2001-05-31) SEQ ID No 1 tables 1,3	1-12, 15-17
X	----- BARTON G J: "PROTEIN SEQUENCE ALIGNMENT AND DATABASE SCANNING" PROTEIN STRUCTURE PREDICTION. A PRACTICAL APPROACH, XX, XX, 1996, pages 31-63, XP000829540 the whole document ----- -/-	1-12, 15-17

☒ Further documents are listed in the continuation of box C.

☒ Patent family members are listed in annex.

* Special categories of cited documents :

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier document but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"&" document member of the same patent family

Date of the actual completion of the international search

3 December 2002

Date of mailing of the international search report

11/12/2002

Name and mailing address of the ISA

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Authorized officer

Keller, Y

INTERNATIONAL SEARCH REPORT

International Application No

PCT/EP 02/07156

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	<p>GEORGE D G ET AL: "CURRENT METHODS IN SEQUENCE COMPARISON AND ANALYSIS" MACROMOLECULAR SEQUENCING AND SYNTHESIS SELECTED METHODS AND APPLICATIONS, XX, XX, 1988, pages 127-149, XP000829541 the whole document</p> <p>---</p>	1-12, 15-17
Y	<p>MADAULE PASCAL ET AL: "A novel partner for the GTP-bound forms of rho and rac" FEBS LETTERS, ELSEVIER SCIENCE PUBLISHERS, AMSTERDAM, NL, vol. 377, no. 2, 1995, pages 243-248, XP002200178 ISSN: 0014-5793 the whole document</p> <p>---</p>	1-12, 15-17
Y	<p>DI CUNTO FERDINANDO ET AL: "Citron Rho-interacting kinase, a novel tissue-specific Ser/Thr kinase encompassing the Rho-Rac-binding protein citron" JOURNAL OF BIOLOGICAL CHEMISTRY, AMERICAN SOCIETY OF BIOLOGICAL CHEMISTS, BALTIMORE, MD, US, vol. 273, no. 45, 6 November 1998 (1998-11-06), pages 29706-29711, XP002170360 ISSN: 0021-9258 the whole document</p> <p>---</p>	1-12, 15-17
Y	<p>NAGASE ET AL: "PREDICTION OF THE CODING SEQUENCE OF UNIDENTIFIED HUMAN GENES. XIII. THE COMPLETE SEQUENCE OF 100 NEW CDNA CLONES FROM BRAIN WHICH CODE FOR LARGE PROTEINS IN VITRO" DNA RESEARCH, UNIVERSAL ACADEMY PRESS, JP, vol. 6, 1999, pages 63-70, XP000952912 ISSN: 1340-2838 the whole document</p> <p>-----</p>	1-12, 15-17

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

Continuation of Box I.2

Claims Nos.: 13, 14 and 15-17 partially

Present claims 13, 14 and 15-17 partially relate to an extremely large number of possible compounds/methods. Support within the meaning of Article 6 PCT and/or disclosure within the meaning of Article 5 PCT is to be found, however, for only a very small proportion of the compounds/products/apparatus/methods claimed. In the present case, the claims so lack support, and the application so lacks disclosure, that a meaningful search over the whole of the claimed scope is impossible.

The applicant's attention is drawn to the fact that claims, or parts of claims, relating to inventions in respect of which no international search report has been established need not be the subject of an international preliminary examination (Rule 66.1(e) PCT). The applicant is advised that the EPO policy when acting as an International Preliminary Examining Authority is normally not to carry out a preliminary examination on matter which has not been searched. This is the case irrespective of whether or not the claims are amended following receipt of the search report or during any Chapter II procedure.

INTERNATIONAL SEARCH REPORT

International application No.
PCT/EP 02/07156

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☒ Claims Nos.: 13, 14 and 15-17 partially
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
see FURTHER INFORMATION sheet PCT/ISA/210
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

PCT/EP 02/07156

Patent document cited in search report		Publication date		Patent family member(s)		Publication date
WO 0138503	A	31-05-2001	AU	1926001 A		04-06-2001
			EP	1240194 A2		18-09-2002
			WO	0138503 A2		31-05-2001
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